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# IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Lal et al.

Title:

HUMAN SOCS PROTEINS

Printed:

Serial No.:

09/701.232

Filing Date:

July 5, 2001

Examiner:

Hamud, F.

Group Art Unit:

1647

Commissioner for Patents

P.O. Box 1450

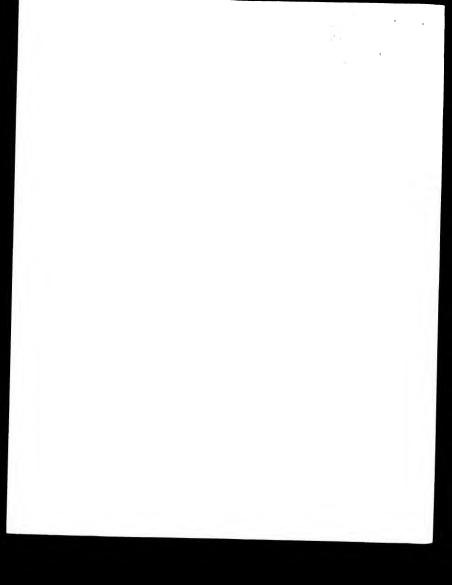
Alexandria, VA 22313-1450

## DECLARATION OF DR. TOD BEDILION UNDER 37 C.F.R. § 1.132

I, TOD BEDILION, a citizen of the United States, residing at 132 Winding Way, San Carlos, California, declare that:

- I was employed by Incyte Corporation (hereinafter "Incyte") as a Director of Corporate Development until May 11, 2001. I am currently under contract to be a Consultant to Incyte Corporation.
- In 1996, I received a Ph.D. degree in Cell, Molecular and Development
   Biology from UCLA. I had previously received, in 1988, a B.S. degree in biology from UCLA.
   Upon my graduation from UCLA, I became, in April 1996, the first employee of
   Synteni, Inc. (hereinafter "Synteni"). I was a Research Director at Synteni from April 1996 until
   Synteni was acquired by Incyte in early 1998.

I understand that Synteni was founded in 1994 by T. Dari Shalon while he was a graduate student at Stanford University. I further understand that Synteni was founded for the purpose of commercially exploiting certain "cDNA microarray" technology that was being worked on at Stanford in the early to mid-1990s. That technology, which I will sometimes refer



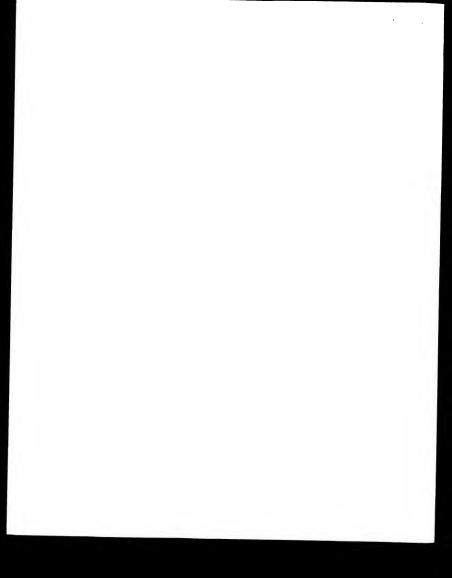
to herein as the "Stanford-developed cDNA microarray technology," was the subject of Dr. Shalon's doctoral thesis at Stanford. I understand and believe that Dr. P.O. Brown was Dr. Shalon's thesis advisor at Stanford.

During the period beginning before I was employed by Synteni and ending upon its acquisition by Incyte in early 1998, I understand Synteni was the exclusive licensee of the Stanford-developed cDNA microarray technology, subject to any right that the United States government may have with respect to that technology. In early 1998, I understand Incyte acquired rights under the Stanford-developed cDNA microarray technology as part of its acquisition of Synteni.

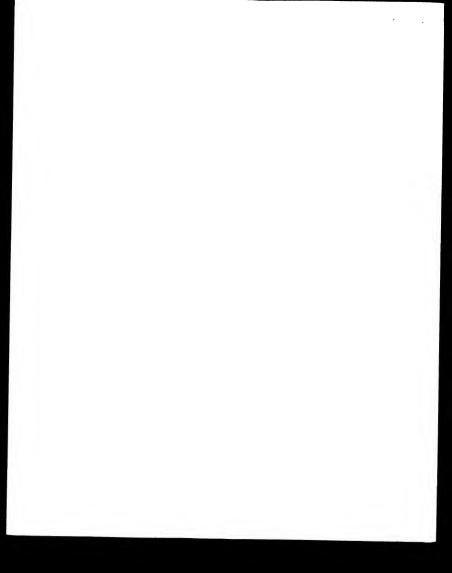
I understand that at the time of the commencement of my employment at Synteni in April 1996, Synteni's rights with respect to the Stanford-developed cDNA technology included rights under a United States patent application that had been filed June 7, 1995 in the names of Drs. Brown and Shalon and that subsequently issued as United States Patent No. 5,807,522 (the Brown '522 patent). In December 1995, the subject matter of the Brown '522 patent was published based on a PCT patent application that had also been filed in June 1995. The Brown '522 patent (and its corresponding PCT application) describes the use of the Stanford-developed cDNA technology in a number of gene expression monitoring applications, as will be discussed more fully below.

Upon Incyte's acquisition of Synteni, I became employed by Incyte. From early 1998 until late 1999, I was an Associate Research Director at Incyte. In late 1999, I was promoted to the position of Director, Corporate Development.

I have been aware of the Stanford-developed cDNA microarray technology since shortly before I commenced my employment at Synteni. While I was employed by Synteni, virtually all (if not all) of my work efforts (as well as the work efforts of others employed by Synteni) were directed to the further development and commercial exploitation of that cDNA microarray technology. By the end of 1997, those efforts had progressed to the point that I understand Incyte agreed to pay at least about \$80 million to acquire Synteni. Since I have been employed by Incyte, I have continued to work on the further development and commercial exploitation of the cDNA microarray technology that was first developed at Stanford in the early to mid-1990s.



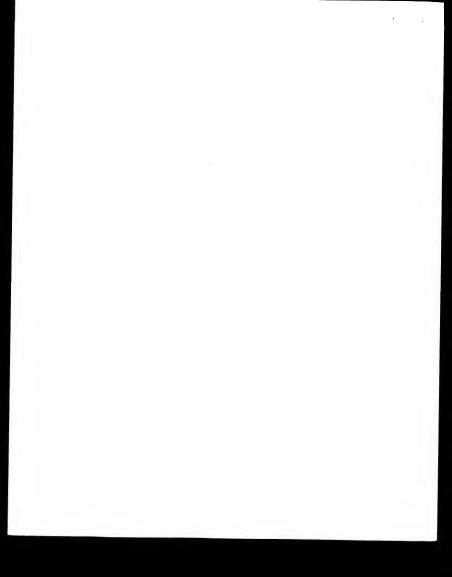
- I have reviewed the specification of a United States patent application that 3 I understand was filed on July 5, 2001 in the names of Preeti Lal et al. and was assigned Serial No. 09/701,232 (hereinafter "the Lal '232 application"). Furthermore, I understand that this United States patent application is the National Stage of International Application No. PCT/US99/11497, filed May 25, 1999, and published in English as WO 99/61614 on December 2, 1999, which claims the benefit under 35 U.S.C. § 119(e) of provisional applications U.S. Ser . No. 60/087,104, filed May 28, 1998 (hereinafter the Lal '104 application) and U.S. Ser. No. 60/150,701, filed December 17, 1998. The provisional applications provide support for what is disclosed in the instant Lal '232 application. The SEQ ID NO:5 and SEQ ID NO:14 sequences recited in the Lal '232 application claims were first disclosed in the Lal '104 application and listed as SEQ ID NO:5 and SEQ ID NO:11, respectively, in the Lal '104 application. My remarks herein will therefore be directed to the Lal '104 patent application, and May 28, 1998, as the relevant date of filing. In broad overview, the Lal '104 specification pertains to certain nucleotide and amino acid sequences and their use in a number of applications, including gene expression monitoring applications that are useful in connection with (a) developing drugs (e.g., for the treatment of cancer, immune disorders, and infectious diseases), and (b) monitoring the activity of drugs for purposes relating to evaluating their efficacy and toxicity.
- 4. I understand that (a) the Lal '232 application contains claims that are directed to an isolated polynucleotide comprising the polynucleotide sequence of SEQ ID NO:14 (hereinafter "the SEQ ID NO:14 polynucleotide"), and (b) the Patent Examiner has rejected those claims on the grounds that the specification of the Lal '232 application does not disclose a specific and substantial asserted utility or a well established utility for the claimed SEQ ID NO:14 polynucleotide. I further understand that whether or not a patent specification discloses a substantial, specific and credible utility for its claimed subject matter is properly determined from the perspective of a person skilled in the art to which the specification pertains at the time of the patent application was filed. In addition, I understand that a substantial, specific and credible utility under the patent laws must be a "real-world" utility.



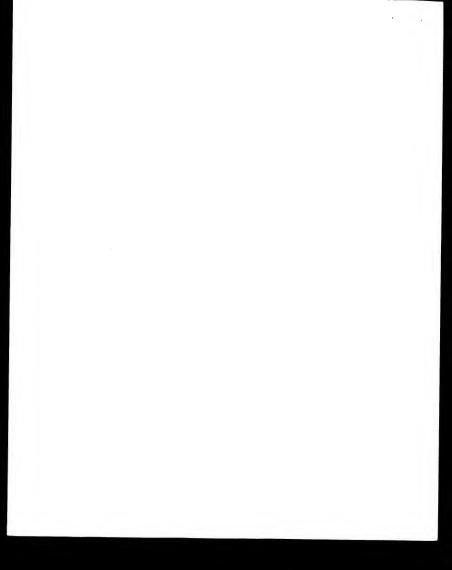
5. I have been asked (a) to consider with a view to reaching a conclusion (or conclusions) as to whether or not I agree with the Patent Examiner's position that the Lal '232 application and its priority application, the Lal '104 application, do not disclose a specific and substantial asserted utility or a well established "real-world" utility for the claimed Lal '232 application SEQ ID NO:14 polynucleotide, and (b) to state and explain the bases for any conclusions I reach. I have been informed that, in connection with my considerations, I should determine whether or not a person skilled in the art to which the Lal '104 application pertains on May 28, 1998 would have concluded that the Lal '104 application disclosed, for the benefit of the public, a specific beneficial use of the Lal '232 application SEQ ID NO:14 polynucleotide in its then available and disclosed form. I have also been informed that, with respect to the "real-world" utility requirement, the Patent and Trademark Office instructs its Patent Examiners in Section 2107.01 of the Manual of Patent Examining Procedure, 8th Edition, August 2001, under the heading I. Specific and Substantial Requirements, Research Tools):

Many research tools such as gas chromatographs, screening assays, and nucleotide sequencing techniques have a clear, specific and unquestionable utility (e.g., they are useful in analyzing compounds). An assessment that focuses on whether an invention is useful only in a research setting thus does not address whether the specific invention is in fact "useful" in a patent sense. Instead, Office personnel must distinguish between inventions that have a specifically identified substantial utility and inventions whose asserted utility requires further research to identify or reasonably confirm.

6. I have considered the matters set forth in paragraph 5 of this Declaration and have concluded that, contrary to the position I understand the Patent Examiner has taken, the specification of the Lal '104 patent application disclosed to a person skilled in the art at the time of its filing a number of substantial, specific and credible real-world utilities for the claimed Lal '232 application SEQ ID NO:14 polynucleotide. More specifically, persons skilled in the art on May 28, 1998 would have understood the Lal '104 application to disclose the use of the Lal '232 application SEQ ID NO:14 polynucleotide in a number of gene expression monitoring applications that were well-known at that time to be useful in connection with the development of drugs and the monitoring of the activity of such drugs. I explain the bases for reaching my conclusion in this regard in paragraphs 7-16 below.



- 7. In reaching the conclusion stated in paragraph 6 of this Declaration, I considered (a) the specification of the Lal '104 application, and (b) a number of published articles and patent documents that evidence gene expression monitoring techniques that were well-known before the May 28, 1998 filing date of the Lal '104 application. The published articles and patent documents I considered are:
- (a) Schena, M., Shalon, D., Heller, R., Chai, A., Brown, P.O., and Davis, R.W., Parallel human genome analysis: Microarray-based expression monitoring of 1000 genes, Proc. Natl. Acad. Sci. USA, 93, 10614-10619 (1996) (hereinafter "the Schena 1996 article") (copy annexed at Tab A);
- (b) Schena, M., Shalon, D., Davis, R.W., Brown, P.O., <u>Quantitative Monitoring of Gene Expression Patterns with a Complementary DNA Microarray</u>, Science, 270, 467-470 (1995) (hereinafter "the Schena 1995 article") (copy annexed at Tab B);
- (c) Shalon and Brown PCT patent application WO 95/35505 titled "Method and Apparatus For Fabricating Microarrays Of Biological Samples," filed on June 16, 1995, and published on December 28, 1995 (hereinafter "the Shalon PCT application") (copy annexed at Tab C);
- (d) Brown and Shalon U.S. Patent No. 5,807,522, corresponding to the Shalon PCT application, titled "Methods For Fabricating Microarrays Of Biological Samples," filed on June 7, 1995 and issued on September 15, 1998 (hereinafter "the Brown '522 patent") (copy annexed at Tab D);
- (e) DeRisi, J., Penland, L., and Brown, P.O. (Group 1); Bittner, M.L., Meltzer, P.S., Ray, M., Chen, Y., Su, Y.A., and Trent, J.M. (Group 2), <u>Use of a cDNA microarray to analyse gene expression patterns in human cancer</u>, Nat. Genet., 14(4), 457-460 (1996) (hereinafter 'the DeRisi article') (copy annexed at Tab E);
- (f) Shalon, D., Smith, S.J., and Brown, P.O., <u>A DNA Microarray System for Analyzing Complex DNA Samples Using Two-color Fluorescent Probe Hybridization</u>, Genome Res., 6(7), 639-645 (1996) (hereinafter "the Shalon article") (copy annexed at Tab F):
- (g) Heller, R.A., Schena, M., Chai A., Shalon, D., Bedilion, T.,
  Gilmore, J., Woolley, D.E., and Davis R.W., <u>Discovery and analysis of inflammatory disease</u>.

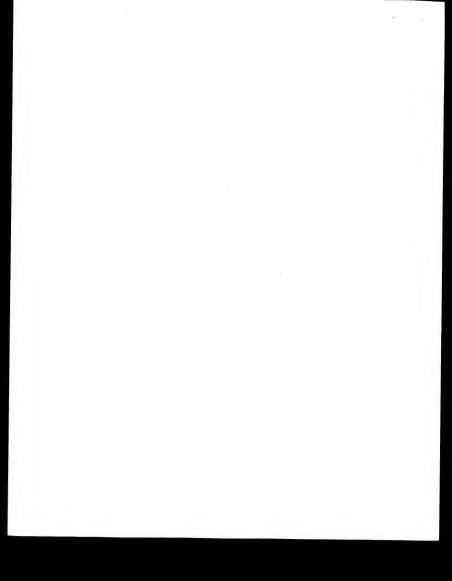


related genes using cDNA microarrays, Proc. Natl. Acad. Sci. USA, 94, 2150-2155 (1997) (hereinafter "the Heller article")(copy annexed at Tab G); and

- (h) Sambrook, J., Fritsch, E.F., Maniatis, T., <u>Molecular Cloning, A</u>
  <u>Laboratory Manual</u>, pages 7.37 and 7.38, Cold Spring Harbor Press (1989) (hereinafter "the Sambrook Manual") (copy annexed at Tab H).
- 8. Many of the published articles and patent documents I considered (i.e., at least items (a)-(f) identified in paragraph 7) relate to work done at Stanford University in the early and mid-1990s with respect to the development of cDNA microarrays for use in gene expression monitoring applications under which Synteni became exclusively licensed. As I will discuss, a person skilled in the art who read the Lal '104 application on May 28, 1998 would have understood that application to disclose the Lal '232 application SEQ ID NO:14 polynucleotide to be useful for a number of gene expression monitoring applications, e.g., as a probe for the expression of that specific polynucleotide in cDNA microarrays of the type first developed at Stanford.

Furthermore, items (a)-(g) establish that gene expression monitoring applications utilizing cDNA microarrays were well-known and established methods routinely used in toxicology testing and drug development at the time of filing the Lal '104 application and for several years prior to May 28, 1998. As such, one of ordinary skill in the art would have recognized that the Lal '232 application SEQ ID NO:14 polynucleotide could be used in toxicology testing and drug development, irrespective of the biochemical activities of the encoded polypeptide.

9. The SEQ ID NO:5 and SEQ ID NO:14 sequences recited in the Lal '232 application claims were first disclosed in the Lal '104 application and listed as SEQ ID NO:5 and SEQ ID NO:11, respectively, in the Lal '104 application. The SEQ ID NO:5 polypeptide is referred to as HSCOP-5 in the Lal '232 application and as SOCP-5 in the Lal '104 application. Turning more specifically to the Lal '104 specification, the SEQ ID NO:5 polypeptide and the SEQ ID NO:11 polynucleotide are shown at pages 46-47 and 51-52, respectively, under the heading "Sequence Listing." The Lal '104 specification specifically teaches that the "invention also provides an isolated and purified polynucleotide comprising a polynucleotide sequence

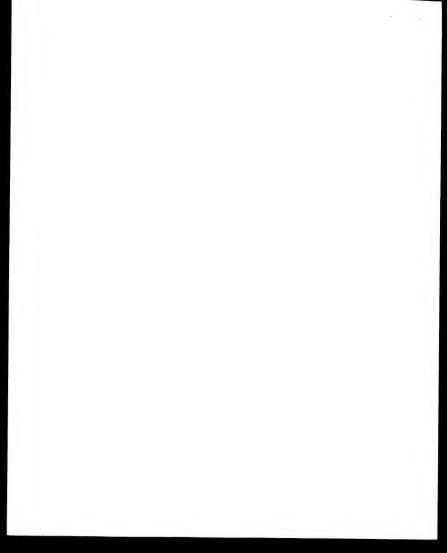


selected from the group consisting of SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12 (SEQ ID NO:7 through 12)..."] (Lal '104 application at page 3, lines 13-15.) It further teaches that (a) the identity of the SEQ ID NO:11 polynucleotide was determined from a uterus tissue cDNA library (UTRSNOR01) (Lal '104 application, Tables 1 and 4), (b) the SEQ ID NO:11 polynucleotide encodes the human SOCS protein (SOCP-5) shown as SEQ ID NO:5 (Lal '104 application at page 2, lines 32-36 and Table 1), and (c) northern analysis of SEQ ID NO:11 shows its expression predominantly in cDNA libraries made from reproductive, cardiovascular, hematopoietic/immune, cancer-associated, inflammation-associated, and fetal tissues (Lal '104 application at Table 3) and therefore "SOCP appears to play a role in cancer, immune disorders, and infectious diseases." (Lal '104 application at page 20, lines 22-23.)

The Lal '104 application discusses a number of uses of the Lal '232 application SEQ ID NO:14 polynucleotide in addition to its use in gene expression monitoring applications. I have not fully evaluated these additional uses in connection with the preparation of this Declaration and do not express any views in this Declaration regarding whether or not the Lal '104 specification discloses these additional uses to be substantial, specific and credible real-world utilities of the Lal '232 application SEQ ID NO:14 polynucleotide. Consequently, my discussion in this Declaration concerning the Lal '104 application focuses on the portions of the application that relate to the use of the Lal '232 application SEQ ID NO:14 polynucleotide in gene expression monitoring applications.

10. The Lal '104 application discloses that the polynucleotide sequences disclosed therein, including the Lal '232 application SEQ ID NO:14 polynucleotide, are useful as probes in microarrays. (Lal '104 application, page 30, line 31 through page 31, line 4 and page 36, line 37 through page 37, line 14.) It further teaches that the microarrays can be used "to monitor the expression level of large numbers of genes simultaneously" for a number of purposes, including "to develop and monitor the activities of therapeutic agents" (Lal '104 application at page 30, lines 31-36).

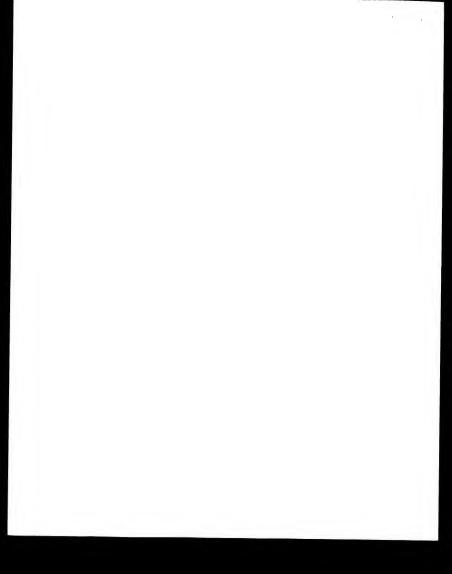
In the paragraph immediately following the Lal '104 teachings described in the preceding paragraph of this Declaration, the Lal '104 application teaches that microarrays can be



prepared using the previously mentioned cDNA microarray technology developed at Stanford in the early to mid-1990s. In this connection, the Lal '104 application specifically cites to the Schena 1996 article identified in item (a) of paragraph 7 of this Declaration (Lal '104 application at page 31, lines 1-2; supra, paragraph 7).

The Schena 1996 article is one of a number of documents that were published prior to the May 28, 1998 filing date of the Lal '104 application that describes the use of the Stanford-developed cDNA technology in a wide range of gene expression monitoring applications, including monitoring and analyzing gene expression patterns in human cancer. In view of the Lal '104 application, the Schena 1996 article, and other related pre-May 28, 1998 publications, persons skilled in the art on May 28, 1998 clearly would have understood the Lal '104 application to disclose the Lal '232 application SEQ ID NO:14 polynucleotide to be useful in cDNA microarrays for the development of new drugs and monitoring the activities of drugs for such purposes as evaluating their efficacy and toxicity, as explained more fully in paragraph 15 below.

With specific reference to toxicity evaluations, those of skill in the art who were working on drug development on May 28, 1998 (and for many years prior to May 28, 1998) without any doubt appreciated that the toxicity (or lack of toxicity) of any proposed drug they were working on was one of the most important criteria to be considered and evaluated in connection with the development of the drug. They would have understood at that time that good drugs are not only potent, they are specific. This means that they have strong effects on a specific biological target and minimal effects on all other biological targets. Ascertaining that a candidate drug affects its intended target, and identification of undesirable secondary effects (i.e., toxic side effects), had been for many years among the main challenges in developing new drugs. The ability to determine which genes are positively affected by a given drug, coupled with the ability to quickly and at the earliest time possible in the drug development process identify drugs that are likely to be toxic because of their undesirable secondary effects, have enormous value in improving the efficiency of the drug discovery process, and are an important and essential part of the development of any new drug. Accordingly, the teachings in the Lal '104 application, in particular regarding use of the Lal '232 application SEQ ID NO:14 polynucleotide in differential gene expression analysis and in the development and the monitoring of the activities of drugs,



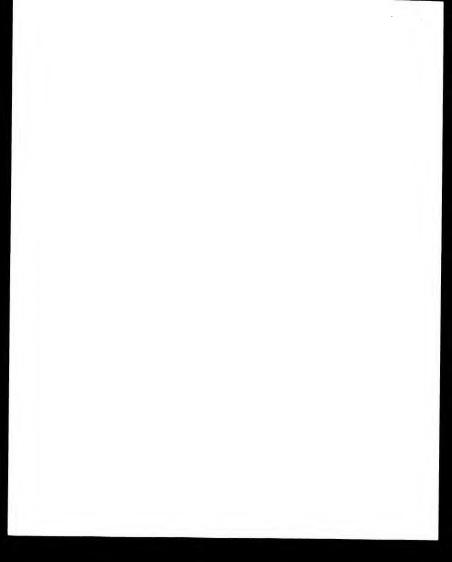
clearly includes toxicity studies and persons skilled in the art who read the Lal '104 application on May 28, 1998 would have understood that to be so.

- 11. The Schena 1996 article was not the first publication that described the use of the cDNA microarray technique developed at Stanford to monitor quantitatively gene expression patterns. More than a year earlier (i.e., in October 1995), the Schena 1995 article, titled "Quantitative Monitoring of Gene Expression Patterns with a Complementary DNA Microarray", was published (see Tabs A and B).
- 12. As previously discussed (*supra*, paragraphs 2 and 7), in the mid-1990s patent applications were filed in the names of Drs. Shalon and Brown that described the Stanford-developed cDNA microarray technology. The two patent documents (i.e., the Shalon PCT application and the Brown '522 patent) annexed to this Declaration at Tabs C and D evidence information that was available to the public regarding the Stanford-developed cDNA microarray technology before the May 28, 1998 filing date of the Lal '104 application.

The Shalon PCT patent application, which was published in December 1995, contains virtually the same (if not exactly the same) specification as the Brown '522 patent. Hence, the Brown '522 patent disclosure was, in effect, available to the public as of the December 1995 publication date of the Shalon PCT application (see Tabs C and D). For the sake of convenience, I cite to and discuss the Brown '522 specification below on the understanding that the descriptions in that specification were published as of the December 28, 1995 publication date of the Shalon PCT application.

The Brown '522 patent discusses, in detail, the utility of the Stanford-developed cDNA microarrays in gene expression monitoring applications. For example, in the "Summary Of The Invention" section, the Brown '522 patent teaches (see Tab D, col. 4, line 52-col. 5, line 8):

Also forming part of the invention is a method of detecting differential expression of each of a plurality of genes in a first cell type, with respect to expression of the same genes in a second cell type. In practicing the method, there is first produced fluorescent-labeled cDNAs from mRNAs isolated from two cells types, where

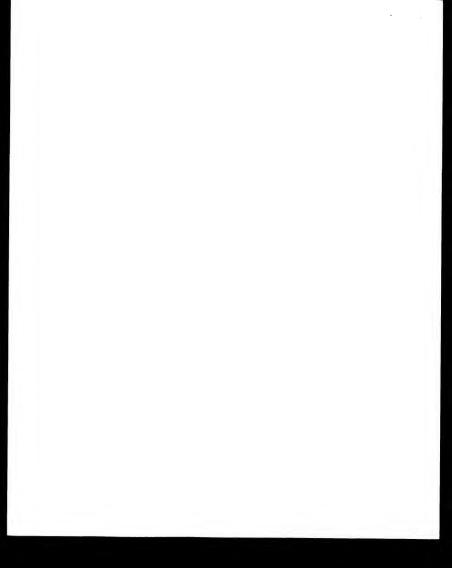


the cDNAs from the first and second cell types are labeled with first and second different flourescent reporters.

A mixture of the labeled cDNAs from the two cell types is added to an array of polynucleotides representing a plurality of known genes derived from the two cell types, under conditions that result in hybridization of the cDNAs to complementary-sequence polynucleotides in the array. The array is then examined by fluorescence under fluorescence excitation conditions in which (i) polynucleotides in the array that are hybridized predominantly to cDNAs derived from one of the first or second cell types give a distinct first and second fluorescence emission color, respectively, and (ii) polynucleotides in the array that are hybridized to substantially equal numbers of cDNAs derived from the first and second cell types give a distinct combined fluorescence emission color, respectively. The relative expression of known genes in the two cell types can then be determined by the observed fluorescence emission color of each spot.

The Brown '522 patent further teaches that the "[m]icroarrays of immobilized nucleic acid sequences prepared in accordance with the invention" can be used in "numerous" genetic applications, including "monitoring of gene expression" applications (see Tab D at col. 14, lines 36-42). The Brown '522 patent teaches (a) monitoring gene expression (i) in different tissue types, (ii) in different disease states, and (iii) in response to different drugs, and (b) that arrays disclosed therein may be used in toxicology studies (see Tab D at col. 15, lines 13-18 and 52-58 and col. 18, lines 25-30).

13. Also pertinent to my considerations underlying this Declaration is the DeRisi article, published in December 1996. The DeRisi article describes the use of the Stanford-developed cDNA microarray technology "to analyze gene expression patterns in human cancer" (see Tab E at, e.g., page 457). The DeRisi article specifically indicates, consistent with what was apparent to persons skilled in the art in December 1996, that increasing the number of genes on the cDNA microarray permits a "more comprehensive survey of gene expression patterns," thereby enhancing the ability of the cDNA microarray to provide "new and useful insights into human biology and a deeper understanding of the gene pathways involved in the pathogenesis of cancer and other diseases" (see Tab E at page 458).

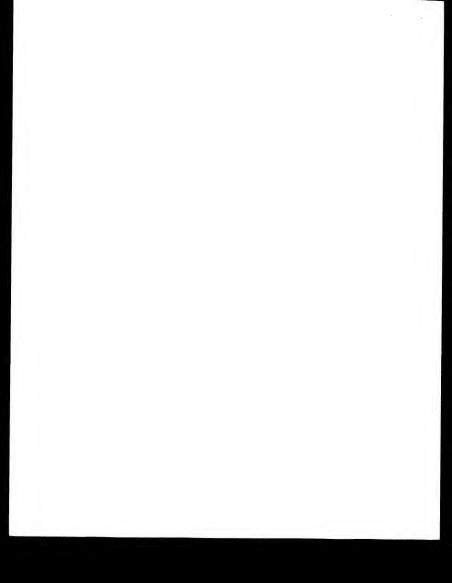


14. Other pre-May 28, 1998 publications further evidence the utility of the cDNA microarrays first developed at Stanford in a wide range of gene expression monitoring applications (see, e.g., the Shalon and the Heller articles at Tabs F and G). By no later than the March 1997 publication of the Heller article, these publications showed that employees of Synteni (i.e., James Gilmore and myself) had used the cDNA microarrays in specific gene expression monitoring applications (see Tab G).

The Heller article states that the results reported therein "successfully demonstrate the use of the cDNA microarray system as a general approach for dissecting human diseases" (Tab G at page 2150). Among other things, the Heller article describes the investigation of "1000 human genes that were randomly selected from a peripheral human blood cell library" and "[t]heir differential and quantitative expression analysis in cells of the joint tissue. . . to demonstrate the utility of the microarray method to analyze complex diseases by their pattern of gene expression" (see Tab G at pages 2150 et seq.).

Much of the work reported on in the Heller article was done in 1996. That article, therefore, evidences how persons skilled in the art were readily able, well prior to May 28, 1998, to make and use cDNA microarrays to achieve highly useful results. For example, as reported in the Heller article, a cDNA microarray that was used in some of the highly successful work reported on therein was made from 1,000 genes randomly selected from a human blood cell library.

application, would understand that application to disclose the Lal '232 application SEQ ID NO:14 polynucleotide, to be highly useful as a probe for the expression of that specific polynucleotide in cDNA microarrays of the type first developed at Stanford. For example, the specification of the Lal '104 application would have led a person skilled in the art on May 28, 1998 who was using gene expression monitoring in connection with working on developing new drugs for the treatment of cancer, immune disorders, and infectious diseases to conclude that a cDNA microarray that contained the Lal '232 application SEQ ID NO:14 polynucleotide would be a highly useful tool and to request specifically that any cDNA microarray that was being used for such purposes contain the Lal '232 application SEQ ID NO:14 polynucleotide. Persons



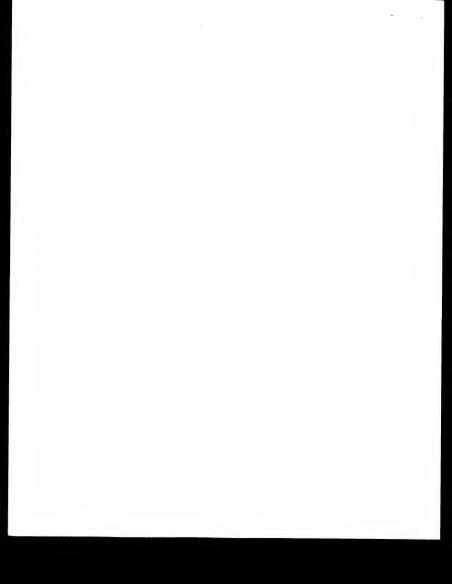
skilled in the art would appreciate that a cDNA microarray that contained the Lal '232 application SEQ ID NO:14 polynucleotide would be a more useful tool than a cDNA microarray that did not contain the Lal '232 application SEQ ID NO:14 polynucleotide in connection with conducting gene expression monitoring studies on proposed (or actual) drugs for treating cancer, immune disorders, and infectious diseases for such purposes as evaluating their efficacy and toxicity.

I discuss in more detail in items (a)-(f) below a number of reasons why a person skilled in the art, who read the Lal '104 specification on May 28, 1998, would have concluded based on that specification and the state of the art at that time, that the Lal '232 application SEQ ID NO:14 polynucleotide would be a highly useful tool for inclusion in cDNA microarrays for evaluating the efficacy and toxicity of proposed drugs for treating cancer, immune disorders, and infectious diseases, as well as for other evaluations:

(a) The Lal '104 application teaches the Lal '232 application SEQ ID NO:14 polynucleotide to be useful as a probe in cDNA microarrays of the type first developed at Stanford. It also teaches that such cDNA microarrays are useful in a number of gene expression monitoring applications, including "to develop and monitor the activities of therapeutic agents [i.e., drugs]" (see paragraph 10, supra).

(b) By May 28, 1998, the Stanford-developed cDNA microarray technology was a well known and widely accepted tool for use in a wide range of gene expression monitoring applications. This is evidenced, for example, by numerous publications describing the use of that cDNA technology in gene expression monitoring applications and the fact that, for over a year, the technology had provided the basis for the operations of an up-and-running company (Synteni), with employees, that was created for the purpose of developing and commercially exploiting that technology (see paragraphs 2, 8 and 10-14, *supra*). The fact that Incyte agreed to purchase Synteni in late 1997 for an amount reported to be at least about \$80 million only serves to underscore the substantial practical and commercial significance, in 1997, of the cDNA microarray technology first developed at Stanford (see paragraph 2, *supra*).

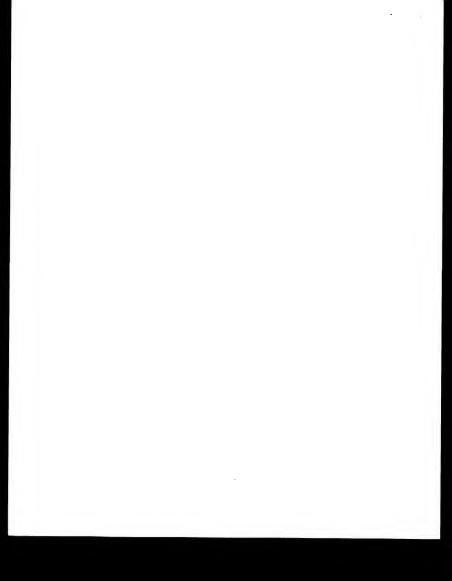
(c) The pre-May 28, 1998 publications regarding the cDNA microarray technology first developed at Stanford that I discuss in this Declaration repeatedly confirm that,



consistent with the teachings in the Lal '104 application, cDNA microarrays are highly useful tools for conducting gene expression monitoring applications with respect to the development of drugs and the monitoring of their activity. Among other things, those pre-May 28, 1998 publications confirmed that cDNA microarrays (i) were useful for monitoring gene expression responses to different drugs (see paragraph 12, *supra*), (ii) were useful in analyzing gene expression patterns in human cancer, with increasing the number of genes on the cDNA microarray enhancing the ability of the cDNA microarray to provide useful information (see paragraph 13, *supra*), and (iii) were a valuable tool for use as part of a "general approach for dissecting human diseases" and for "analyz[ing] complex diseases by their pattern of gene expression" (see paragraph 14, *supra*).

(d) Based on my own extensive work for a company whose business was the development and commercial exploitation of cDNA microarray technology for more than two years prior to the May 28, 1998 filing date of the Lal '104 application, I have first-hand knowledge concerning the state of the art with respect to making and using cDNA microarrays as of May 28, 1998 (see paragraphs 2 and 14, *supra*). Persons skilled in the art as of that date would have (a) concluded that the Lal '104 application disclosed cDNA microarrays containing the Lal '232 application SEQ ID NO:14 polynucleotide to be useful, and (b) readily been able to make and use such microarrays with useful results.

(e) The Lal '104 specification contains a number of teachings that would lead persons skilled in the art on May 28, 1998 to conclude that a cDNA microarray that contained the Lal '232 application SEQ ID NO:14 polynucleotide would be a more useful tool for gene expression monitoring applications relating to drugs for treating cancer, immune disorders, and infectious diseases than a cDNA microarray that did not contain the Lal '232 application SEQ ID NO:14 polynucleotide. Among other things, the Lal '104 specification teaches that the identity of the Lal '232 application SEQ ID NO:14 polynucleotide (listed as SEQ ID NO:11 in the Lal '104 application) was determined from a uterus tissue cDNA library (UTRSNOR01) (Lal '104 application, Tables 1 and 4). Moreover, northern analysis of Lal '232 application SEQ ID NO:14 polynucleotide (listed as SEQ ID NO:11 in the Lal '104 application) shows its expression predominantly in cDNA libraries made from reproductive, cardiovascular, hematopoietic/immune, cancer-associated, inflammation-associated, and fetal tissues (Lal '104

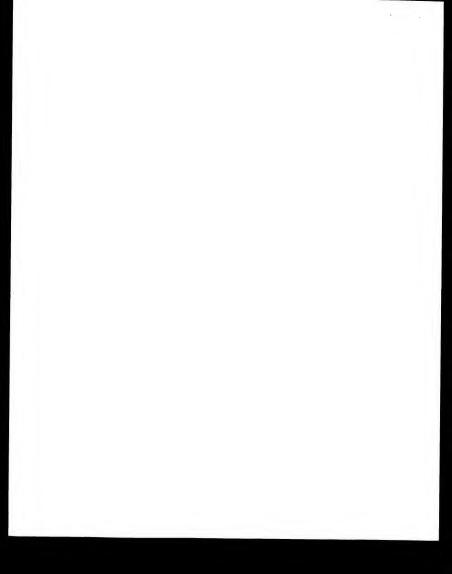


application at Table 3) and therefore "SOCP appears to play a role in cancer, immune disorders, and infectious diseases." (Lal '104 application at page 20, lines 22-23.). (See paragraph 9, supra).

(f) Persons skilled in the art on May 28, 1998 would have appreciated (i) that the gene expression monitoring results obtained using a cDNA microarray containing a probe to the Lal '232 application SEQ ID NO:14 polynucleotide would vary, depending on the particular drug being evaluated, and (ii) that such varying results would occur both with respect to the results obtained from the probe described in (i) and from the cDNA microarray as a whole (including all its other individual probes). These kinds of varying results, depending on the identity of the drug being tested, in no way detracts from my conclusion that persons skilled in the art on May 28, 1998, having read the Lal '104 specification, would specifically request that any cDNA microarray that was being used for conducting gene expression monitoring studies on drugs for treating cancer, immune disorders, and infectious diseases (e.g., a toxicology study or any efficacy study of the type that typically takes place in connection with the development of a drug) contain the Lal '232 application SEQ ID NO:14 polynucleotide as a probe. Persons skilled in the art on May 28, 1998 would have wanted their cDNA microarray to have a probe as described in (i) because a microarray that contained such a probe (as compared to one that did not) would provide more useful results in the kind of gene expression monitoring studies using cDNA microarrays that persons skilled in the art have been doing since well prior to May 28, 1998.

The foregoing is not intended to be an all-inclusive explanation of all my reasons for reaching the conclusions stated in this paragraph 15, and in paragraph 6, *supra*. In my view, however, it provides more than sufficient reasons to justify my conclusions stated in paragraph 6 of this Declaration regarding the Lal '104 application disclosing to persons skilled in the art at the time of its filing substantial, specific and credible real-world utilities for the Lal '232 application SEQ ID NO:14 polynucleotide.

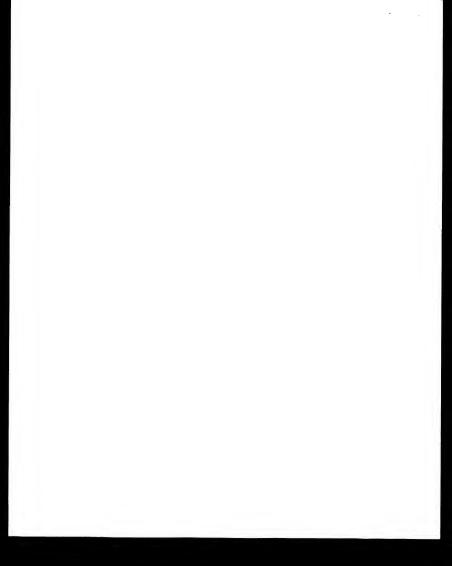
16. Also pertinent to my considerations underlying this Declaration is the fact that the Lal '104 disclosure regarding the uses of the Lal '232 application SEQ ID NO:14 polynucleotide for gene expression monitoring applications is not limited to the use of that



polynucleotide as a probe in microarrays. For one thing, the Lal '104 disclosure regarding the hybridization technique used in gene expression monitoring applications is broad. (Lal '104 application at, e.g., page 4, lines 12-21.) In addition, the Lal '104 specification repeatedly teaches that the polynucleotides described therein (including Lal '232 application SEQ ID NO:14 polynucleotide) may desirably be used as probes in any of a number of long established "standard" non-microarray techniques, such as northern analysis, for conducting gene expression monitoring studies. See, e.g.:

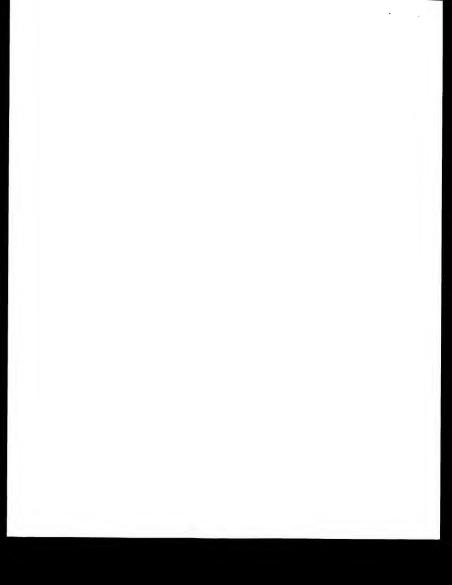
- (a) Lal '104 application at page 7, lines 29-31 ("Northern analysis is indicative of the presence of nucleic acids encoding SOCP in a sample, and thereby correlates with expression of the transcript from the polynucleotide encoding SOCP.");
- (b) Lal '104 application at page 29, lines 25-28 ("The polynucleotide sequences encoding SOCP may be used in... Northern analysis, dot blot, or other membrane-based technologies... Such qualitative or quantitative methods are well known in the art"):
- (c) Lal '104 application at page 30, lines 1-6 ("In order to provide a basis for the diagnosis of a disorder associated with expression of SOCP, a normal or standard profile for expression is established. This may be accomplished by combining body fluids or cell extracts taken from normal subjects, . . . with a sequence, or a fragment thereof, encoding SOCP, under conditions suitable for hybridization or amplification. Standard hybridization may be quantified by comparing the values obtained from normal subjects with values from an experiment in which a known amount of a substantially purified polynucleotide is used.") (emphasis supplied); and
- (d) Lal '104 application at page 34, lines 13-16 ("Northern analysis is a laboratory technique used to detect the presence of a transcript of a gene and involves the hybridization of a labeled nucleotide sequence to a membrane on which RNAs from a particular cell type or tissue have been bound. (See, e.g., Sambrook, supra, ch. 7; and Ausubel, supra, ch. 4 and 16.)"

The "Sambrook et al." reference cited in item (d) immediately above is a reference that was well known to persons skilled in the art on May 28, 1998. A copy of pages from that reference manual, which was published in 1989, is annexed to this Declaration at Tab H. The



attached pages from the Sambrook manual provide an overview of northern analysis and other membrane-based technologies for conducting gene expression monitoring studies that were known and used by persons skilled in the art for many years prior to the May 28, 1998 filing date of the Lal '104 application.

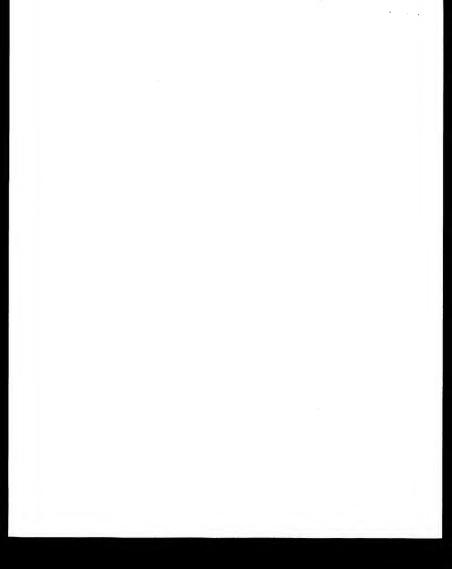
A person skilled in the art on May 28, 1998, who read the Lal '104 specification, would have routinely and readily appreciated that the Lal '232 application SEQ ID NO:14 polynucleotide disclosed therein would be useful as a probe to conduct gene expression monitoring analyses using northern analysis or any of the other traditional membrane-based gene expression monitoring techniques that were known and in common use many years prior to the filing of the Lal '104 application. For example, a person skilled in the art on May 28, 1998 would have routinely and readily appreciated that the Lal '232 application SEQ ID NO:14 polynucleotide would be a useful tool in conducting gene expression analyses, using the northern analysis technique, in furtherance of (a) the development of drugs for the treatment of cancer, immune disorders, and infectious diseases, and (b) analyses of the efficacy and toxicity of such drugs.



17. I declare further that all statements made herein of my own knowledge are true and that all statements made herein on information and belief are believed to be true; and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, and that willful false statements may jeopardize the validity of this application and any patent issuing thereon.

| Tod Bedilion |  |
|--------------|--|
|              |  |

| Signed at   | , California |
|-------------|--------------|
| this day of | 2003         |



## Parallel human genome analysis: Microarray-based expression monitoring of 1000 genes

(Human Genome Project / DNA chin / sens discovery /T cell)

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Contributed by Ronald W. Davis, June 26, 1996

Microarrays containing 1046 human cDNAs of unknown sequence were printed on glass with high-speed robotics. These 1.0-cm2 DNA "chips" were used to quantitatively monitor differential expression of the cognate human genes using a highly sensitive two-color hybridization assay. Array elements that displayed differential expression patterns under given experimental conditions were characterized by sequencing. The identification of known and novel heat shock and phorbol ester-regulated genes in human T cells demonstrates the sensitivity of the assay. Parallel gene analysis with microarrays provides a rapid and efficient method for largescale human gene discovery.

Biology has entered the genome era (1). Complete genome sequences for all of the model organisms and human will probably be available by the year 2003 (2). Torrents of human expressed sequence tags (ESTs) provide a starting point for elucidating the function of tens of thousands of cognate genes (3). Genome analysis will provide insights into growth, development, differentiation, homeostasis, aging, and the onset of diseases (1-3). A detailed understanding of the human genome will require the implementation of sophisticated methods for gene expression analysis and gene discovery.

Recently, a microarray-based method for high-throughput monitoring of plant gene expression was described (4). This "chip"-based approach involved using microarrays of cDNA clones as gene-specific hybridization targets to quantitatively measure expression of the corresponding plant genes (4, 5). A two-color fluorescence labeling and detection scheme facilitated sensitive differential expression analysis of different plant tissues (4, 5). The efficiency of this approach for studies in higher plants suggested the use of this method for human genome analysis (4-7). Here, we report the use of cDNA microarrays for human gene expression monitoring, biological investigation, and gene discovery.

#### MATERIALS AND METHODS

Human eDNA Clones. The cDNA library was made with mRNA from human peripheral blood lymphocytes transformed with the Epstein-Barr virus. Inserts >600 bp were cloned into the lambda vector AYES-R to generate 107-108 recombinants. Bacterial transformants were obtained by infecting E. coli strain JM107/AKC. Colonies were pieked at random and propagated in a 96-well format, and minilysate DNA was prepared by alkaline lysis using REAL preps (Qiagen, Chatsworth, CA). Inserts were amplified by PCR in 96-well format using primers (PAN132, 5'-CCTC-TATACTTTA ACGTCA AGG; and PAN133, 5'-TTGTGTG-GAATTGTGAGCGG) complementary to the AYES polylinker and containing a six-carbon amino modification (Glen Research, Sterling, VA) on the 5' end, PCR products were purified in a 96-well format using QIAquick columns (Oiagen).

Microarray Preparation. Amino-modified PCR products were suspended at a concentration of 0.5 mg/ml in 3× standard saline citrate (SSC) and arrayed from 96-well microtiter plates onto silvlated microscope slides (CEL Associates. Houston) using high-speed robotics (4-7). A total of 1056 cDNAs, representing 1046 human clones and 10 Arabidopsis controls, were arrayed in 1.0-cm2 areas. Printed arrays were incubated for 4 hr in a humid chamber to allow rehydration of the array elements and rinsed, once in 0.2% SDS for 1 min. twice in H2O for 1 min, and once for 5 min in sodium borohydride solution (1.0 g of NaBH4 dissolved in 300 ml of PBS and 100 ml of 100% ethanol). The arrays were submerged in H<sub>2</sub>O for 2 min at 95°C, transferred quickly into 0.2% SDS for 1 min, rinsed twice in H-O, air dried, and stored in the dark

Fluorescent Probes. Tissue mRNAs were purchased (CLONTECH). Jurkat mRNA was isolated as described by Schena et al. (4). Probes were made as described (4) with several modifications. The reverse transcriptase used here was Superscript II RNase H- (GIBCO). The Cv5-dCTP was purchased from Amersham. Each reverse transcription reaction contained 3.0 µg of total human mRNA. Arabidopsis control mRNAs were made by in vitro transcription of cloned HAT4, HAT22, and YesAt-23 cDNAs (4, 8, 9) using an RNA Transcription Kit (Stratagene). For quantitation, the mRNAs were doped into the reverse transcription reaction at ratios of 1:100,000, 1:10,000, and 1:1000 (wt/wt) respectively. Following the reverse transcription step, samples were treated with 2.5 µl of 1 M sodium hydroxide for 10 min at 37°C, then neutralized by adding 2.5 µl of 1 M Tris-HCl (pH 6.8) and 2.0 µl of 1 M HCI. Probe mixtures contained cDNA products derived from 3 µg of total mRNA, suspended in 5.0 µl of hybridization buffer (5× SSC plus 0.2% SDS).

Hybridization and Seanning, Probes were hybridized to 1.0-cm² microarrays under a 14 × 14 mm glass coverslip for 6-12 hr at 60°C in a custom-built hybridization chamber (4-7). Arrays were washed for 5 min at room temperature (25°C) in low stringency wash buffer (1× SSC/0.2% SDS), then for 10 min at room temperature in high stringency wash buffer (0.1× SSC/0.2% SDS). Arrays were scanned in 0.1× SSC using a fluorescence laser scanning device (4-7), fitted with a custom filter set (Chroma Technology, Brattleboro, VT). Accurate differential expression measurements (i.e., final fluorescence ratios) were obtained by taking the average of the ratios of two independent hybridizations.

Abbreviation: EST, expressed sequence tag.

Data deposition: The sequences reported in this paper have been deposited in the GenBank data base (accession nos. U56654-U56660). To whom reprint requests should be addressed, e-mail: schena@ cmgm.stanford.edu.

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Cell Culture. Jurkat cells were grown in a tissue culture incubator (37°C and 5% CO<sub>2</sub>) in RPMI medium supplemented with 10% fetal bovine serum. 100 µg of streptomycin per ml. and 500 units of penicillin per ml. Heat shock corresponded to a 4-hr incubation at 43°C. Phorbol ester treated cells were grown for 4 hr in the presence of 50 ng of phorbol 12-myristate 13-acetate (PMA) per ml.

RNA Blotting. Dot blots were performed as described (4). DNA Sequencing. Sequences were obtained using the PAN132 and PAN133 primers and a 373A automated sequencer, according to the instructions of the manufacturer (Applied Biosystems)

Computer Graphics and Informatics. Pseudocolor representations of fluorescent images were made with National Institutes of Health tMAGE software (version 1.52). Software for differential expression representations was purchased from Imaging Research (St. Catherine's, ON, Canada). Sequence searches were made to the nonredundant nucleotide data base at the National Center for Biotechnology Information (NCBI) using Macintosh BLAST software. The EST data base was accessed via the World Wide Web (http://www.ncbi.nlm.nih.gov/).

### RESULTS

Gene Discovery and the Heat Shock Response. Microarrays were used to examine the heat shock response in cultured human T (Jurkat) cells. Control (37°C) and heat-treated (43°C) cells were harvested and lysed, and total mRNA from the two cell samples was labeled by reverse transcriptase incorporation of fluorescein- and Cv5-dCTP, respectively. In a second set of labeling reactions, the fluorescent groups were 'swapped' such that samples from control and heat-treated

samples were labeled with Cy5- and fluorescein-dCTP, respectively. Each pair of fluorescent probes was hybridized to a 1056-element microarray. The arrays were washed at high stringency and scanned with a confocal laser scanning device to detect emission of the two fluorescent groups

Hybridization signals were observed to >95% of the human cDNA array elements, but not to any of the Arabidopsis negative controls (Fig. 1). Fluorescence intensities spanned more than three orders of magnitude for the 1046 array elements surveyed (Fig. 1). Comparative expression analysis of heat shocked versus control cells in the two experiments revealed 17 array elements that displayed altered fluorescence ratios of ≥2.0-fold (Figs. 1 and 24). Of the 17 putative differentially expressed genes. 11 were induced by heat shock treatment and 6 displayed modest repression (Figs. 1 and 2.4).

To determine the identity of the heat-regulated genes. cDNAs corresponding to each of the 17 array elements were sequenced on the proximal and distal end. Data base searches revealed perfect matches for 14 of the 17 clones, and in each case proximal and distal cDNA sequences mapped to the same gene (Table 1). Of the 1046 human genes examined on the microarray, the five most highly induced in heat-treated cells were heat shock protein 90α (hsp90α), dnaJ, hsp90β, polyubiquitin, and t-complex polypeptide-1 (tcp-1) (Table 1). Three of the 17 clones did not match any entry in the public data base, though one of the clones (B7) exhibited significant homology to an EST from Caenorhabditis elegans (Table 1). Each of the novel sequences (B7-B9) exhibited = 2-fold induction (Table 1) and relatively low-level expression (Table 2).

To confirm the microarray results, mRNA levels for each of the genes were measured by RNA blotting. Each of the genes that displayed heat shock induction, including the three novel

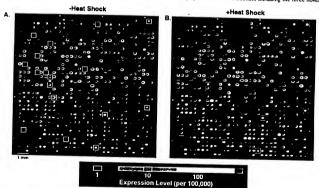
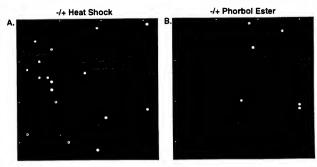


Fig. 1. Human gené expression monitored on a microarray. Fluorescent scans represented in a pseudocolor scale correspond to expression levels The array contains 10 Araphdopsia controls (upper left corner, elements 1-10) and 1046 human perspheral blood cDNAs. Fluorescent probes were prepared by labeling mRNA from Jurkas cells grown as 37°C (-Heat Shock, A) or 43°C (+Heat Shock, B). Array elements had display altered fluorescent miensity (white boxes) corresponded to genes activated (red boxes) or repressed (green boxes) by heat shock. The color bar was calibrated in separate experiments using known quantities (w/w) of Arabidopsis control mRNAs added to the labeling reaction. Microarray rows (a) left) and columns (a) the top) are demarcated at 10 element increments (white circles). (Bar = 1 mm.)



# :: <0.5 | 0.5 - 2.0 >2.0

### **Expression Ratios**

Fig. 2. Elemental displays of activated and repressed genes. Fluorescence ratios of two-color microarray scans (Fig. 1) are depicted schematically. Fluorescen-labeled probes from Jurkat cells subjected to (4) heat shock or (8) phorbol ester treatment were compared with CS-slabeled probes from untertacted cells. In a second set of reactions, the fluorescent groups were exapped (see text). The data represental the average of the ratios from two hybridations, excluding values in which the difference of the two ratios was greater than half the average ratio. The color bar corresponds to expression ratios, with are independent of the absolute expression level of a given gene.

Table 1. Microarray elements corresponding to differentially expressed genes

| Clone | Row | Column | Ratio | Blast identity                | Accession no.  |
|-------|-----|--------|-------|-------------------------------|----------------|
| Bi    | 24  | 21     | 0.5   | CYC oxidase III               | J01415, J01415 |
| B2    |     | 31     | 0.5   | β-Actin                       | NR, X00351     |
| B3    | 15  | 8      | 0.5   | CYC oxidase 111               | J01415, J01415 |
| B4    | 32  | 19     | 0.5   | CYC oxidase 111               | J01415, J01415 |
| B5    | 17  | 8      | 0.5   | CYC oxidase III               | J01415, J01415 |
| B6    | 22  | 31     | 0.5   | B-Actin                       | NR. X00351     |
| B7*   | 5   | 4      | 2.0   | Novel*                        | U56653, U5665- |
| B8    | 2   | 19     | 2.0   | Novel <sup>†</sup>            | U56655, U5665  |
| B9    | 14  | 5      | 2.2   | Novel*                        | U56657, U5665  |
| B10   | 7   | 8      | 2.4   | Polyubiquitin                 | X04803, X0480  |
| B11   | 12  | 2      | 2.4   | TCP-1                         | X52882, X5288  |
| B12   | 28  | 2      | 2.5   | Polyubiquitin                 | M17597, M1759  |
| B13   | 14  | 7      | 2.5   | Polyubiquitin                 | X04803, X0480  |
| B14   | 20  | 9      | 2.6   | HSP90B                        | M16660, M1666  |
| B15   | 30  | 12     | 4.0   | DnaJ homolog                  | D13388, D1338  |
| B16   | 10  | 5      | 5.8   | HSP90a                        | X07270, X0727  |
| B17   | 13  | 16     | 6.3   | HSP90a                        | M27024, X1518  |
| B18   | - ; | 19     | 2.0   | β <sub>2</sub> -microglobulin | \$54761, M3068 |
| B19   | 21  | 30     | 2.1   | Novel*                        | U56659, U5666  |
| B20   | -3  | 26     | 2.2   | 6microglobulin                | \$54761, M3068 |
| B21   | í   | 18     | 2.6   | PGK                           | M11968, L0016  |
| B22   | 22  | 30     | 3.5   | NF-«B1                        | Z47744, M5564  |
| B23   | 20  | 16     | 19    | PAC-1                         | L11329, L11329 |

Come, name, army position (Fig. 1). (Issuescence raiso, sequence identity, and accession number of CDNAs that manifested addifferential expression opations with protest prepared from heat shock. (Fig. 1) and prothost insert-intered (Bit 8:2). Jurkas cells. Clones showing >98% identity over 300 nucleouides were assumed to be identical to known sequences. All genes are nuclear exercit CVC outdates III (municipondines). Accession number of reflex the highest score for protumal and distalt sequence traces, respectively. CVC, evidentime et TCP-1. T-complex polypeptide. HSP, heat shock protein. PGL phosphagistee rate viaus. When the control of the protein of a derivated cells, and MR. trace not readile due to the proteins of the protein of the proteins of the pr

poly(A) + tract.
\*B7 is 67% identical to an EST from C. elegans (D76026).

<sup>\*</sup>No match in the public data bases

Table 2. Human gene expression monitored by microarray and RNA blot analyses

|            |                               | Expression level, per 10 <sup>s</sup> mRNAs |      |          |       |  |  |
|------------|-------------------------------|---|------|----------|-------|--|--|
| Clone      | Blast identity                | Містоагтау                                  | Rano | RNA bioi | Ratio |  |  |
| Bl         | CYC oxidase III               | 92/46                                       | 0.5  |          |       |  |  |
| B2         | β-Actin                       | 240/120                                     | 0.5  | 100/80   | 0.8   |  |  |
| B3         | CYC oxidase III               | 36/18                                       | 0.5  | 270/280  | 1.0   |  |  |
| B4         | CYC oxidase III               | 76/38                                       |      | ND       | ND    |  |  |
| B5         | CYC oxidase III               | 62/31                                       | 0.5  | ND       | ND    |  |  |
| <b>B</b> 6 | β-Actin                       |   | 0.5  | ND       | ND    |  |  |
| B7         | Novel (weakly to D76026)      | 180/89                                      | 0.5  | ND       | ND    |  |  |
| Bß         | Novel                         | 1.3/2.6                                     | 2.0  | 0.77/1.8 | 2.3   |  |  |
| B9         | Novel                         | 2.0/4.0                                     | 2.0  | 1.5/3.4  | 2.3   |  |  |
| B10        | Polyubiquitin                 | 0.8/1.8                                     | 2.2  | 1.2/1.8  | 1.5   |  |  |
| B11        | TCP-1                         | 0.8/1.9                                     | 2.4  | 25/89    | 3.6   |  |  |
| B12        |                               | 2.3/5.5                                     | 2.4  | 7.1/27   | 3.8   |  |  |
| B13        | Polyubiquitin                 | 0.8/2.0                                     | 2.5  | ND       | ND    |  |  |
| B14        | Polyubiquitin                 | 1.7/4.3                                     | 2.5  | ND       | ND    |  |  |
| B15        | HSP908                        | 75/200                                      | 2.6  | 30/120   | 4.0   |  |  |
|            | DnaJ homolog                  | 1.0/4.0                                     | 4.0  | 1.6/13   |       |  |  |
| B16        | HSP90a                        | 0.6/3.5                                     | 5.8  | 3.2/29   | 8.1   |  |  |
| B17        | HSP90a                        | 0.8/5.0                                     | 6.3  |          | 9.1   |  |  |
| B18        | β <sub>2</sub> -microglobulin | 1.0/2.0                                     | 2.0  | 8.6/62   | 7.2   |  |  |
| B19        | Novel                         | 1.2/2.5                                     | 2.1  | 5.4/15   | 2.8   |  |  |
| B20        | β₂-microglobulin              | 2.7/5.9                                     | 2.1  | 4.5/9.5  | 2.5   |  |  |
| B21        | Phosphoglycerate kinase       | 2.4/6.2                                     |      | ND       | ND    |  |  |
| B22        | NF-KB1                        | 1.7/6.0                                     | 2.6  | 4.7/9.2  | 2.0   |  |  |
| B23        | PAC-1                         | 0.5/9.5                                     | 3.5  | 0.65/4.7 | 7.2   |  |  |
| Chama      |                               | 0.5/9.5                                     | 19   | 0.21/15  | 71    |  |  |

Shown are expression levels per 100,000 mRNAs (wi/wt) of genes assaved with a microarray (Fig. 1) or RNA blot Ratio correspond to values from cells subjected to heat shock (Bi-17) or phorbot ester treatment (BiB-23) relative to untersaid cells. Clone and gene namest are given in Table 1. ND, not determined.

sequences, exhibited elevated mRNA levels by dot blot analysis (Table 2). In all cases, expression raives as determined by the two procedures differed by <2.00 flor in the gases identified in the heast shock experiments (Table 2). The two assays differed more widely in terms of assessing absolute expression levels; nonchelects absolute expression and the contraction of th

Phorbol Ester Signaling. To explore a signaling pathway distinct from the heat shock response, microarrays were used to examine the cellular effects of phorbol ester treatment. Jurkat cells were treated with phorbol ester, harvested, lysed, and used as a source of mRNA Samples of mRNA from untreated or phorbol ester-stimulated cells were labeled with reverse transcriptase. The probes were mixed, hybridized to microarrays, and scanned for fluorescence emission of the two fluorescent groups. A total of its array elements displayed ≥2.0-fold elevated signals with probes from phorbol ester-treated cells relative to control samples (Fig. 2B).

To determine the identity of implies (Fig. 29). To determine the identity of implies (Fig. 29) ester-induced genes, clones corresponding to the time of the execution of the ex

Transcript Imaging in Human Tissues. To determine whether microarrays could be used to monitor expression in human tissues, probes were prepared from human bone mar-

row, brain, prostate, and heart by tabeling each mRNA sample with Cy5-dCTP. In a separate reaction, a control probe was prepared by labeling Jurkat mRNA similar download an aliquot of the fluorescein-dCTP. The four Cy5-slabeled probes were and many the fluorescein-tabeled control samples are fluorescein-tabeled control samples the fluorescein-tabeled control samples with the fluorescein-tabeled control samples are more arrays. The fluorescein-tabeled control samples are more arrays are the fluorescein control to generate an expression, and hybrid-zation signals for each of the tissues samples were normalized to the Jurkat control to generate an expression profile for each of the 1046 clones present on the array.

Detectable expression was observed for all 15 of the heat shock and phorbol exterved may observed for all 15 of the heat shock and phorbol exterved may be seen as the four tissue types examined (Fig. 3). In general, the consistent of expression in the four tissues (Table 2). In general, the consistent of the four tissues (Table 2), in general the consistent of the four tissues (Table 2). Seen the four tissues (Table 2), were highly expressed in bone marrow. Frain, prostate, and heart (Fig. 24). Expression of cytochrome c oxidase, the two marrow, brain, prostate, and heart (Fig. 24). Expression of cytochrome c oxidase, hispon, and the novel B7 sequence was significantly greater in heart than in the other tissues (Fig. 23).

#### DISCUSSION

Many of the heat shock genes identified in this study encode factors that function either as molecular phaperones' (HSP906, HSP906, Dnal, TCP-1) or as medicines of protein degradation (probublequium). The identification are shocked induction (10-15). Proteins undergo denautroin are shocked induction (10-15). Proteins undergo denautroin are shocked temperatures, and those that fail to maintain proper conformation must be selectively degraded (10-15). It will be interesting to determine whether the three novel heat shock-inducible sequences (BT-B9) mediate protein folding and turnover or possess some other biochemical activity. Complete nucleotide sequence determination. Conceptual translation, expression monitoring, and biochemical analysis should provide a detailed functional understanding of these genes.

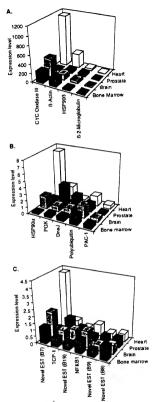


Fig. 3. Transcript profiles of heat shock and phorbol esterregulated genes. Gene expression levels per 100,000 mRNNa (r-aves) are shown for 15 genes (Table 1) in human bone marrow (red.) brain (green), prostate (blue), and heart (yellow). Genes are grouped according to expression levels (4-4-C).

Phorbol ester, a potent activator of protein kinase C (16, 17). induced a set of genes distinct from those involved in the heat shock pathway. The most highly induced gene identified in this study. PAC-1, encodes a nuclear tyrosine kinase that may play a role in regulating transcription and cell cycle progression (18). NF-xBl, a second phorbol ester-inducible gene, is an intensively studied member of the Rel transcription factor family (19-21). The Rel proteins are activated by a large number of stimuli, including phorbol esters, cytokines, bacterial and viral pathogens, and ultraviolet light (19-21). Modest activation was observed for three sequences not known to be inducible by phorbol esters, including phosphoglycerate kinase, β2-microglobulin, and a novel human gene (B19). Extensive expression monitoring with microarrays should assist in understanding how each of these genes integrate into the highly complex phorbol ester signaling pathway.

It is striking that four novel human genes were discovered with an array of 1000 randomly chosen clones, particularly because the heat shock and photobol ester signaling pathways have been so intensively studied (10–21). The facile discovery of these sequences underscores the fact that microarrays can be used for gene discovery in the absence of any sequence information. By this approach, clones are chosen at random from any library of interest and only those clones that display interesting expression patterns are sequenced and characterized. This parallel assay, coupled with a modest DNA sequencing facility, allows high-throughput human genome expression

analysis and gene discovery.

Genes that are activated or repressed by a given stimulus provide Dentity of the Cellular pathway involved activated to the Cellular pathway involved activated activation of these gene expression "signatured" can provide a dynamic view of the mode of action of a given signaling substance (22-24). Microarrays may thus allow rapid mechanistic examination of hormones, drugs, elicitors, and other small molecules, moreover, functional analysis of transcription factors, kinases, growth factors, cyto-kines, receptors, and other gene products should be possible. Efforts are underways to develop mRNA amplification strategies to enable probe preparation from minute tissue stamping that the product of the control of the control

ing in a clinical setting. The current indecision limit of the assay allows monitoring of transcripts that represent ~1:500.000 (wt/wt) of the total mRNA. This 10-toid increase in sensitivity compared with the original report (4) was achieved largely by modifying the coupling chemistry, which reduced background fluorescence. The significance of this improvement is considerable in that approximately half the human genes identified in this study, including all four novel sequences, exhibited expression levels below the original detection limit of 1:50.000 (esson levels below the original detection limit of 1:50.000 the

The ability to detec 2/old changes in expression was achieved by the use of the color function of the labeling and detection scheduled the color of the color of

Microarrays offer a number of advantages over other potential high-capacity approaches to expression analysis. The high-capacity approaches to expression analysis. The straightful of the capacity of the capacity of the capacity array dentities, and the use of fluorescence labeling and detection schemes. These features provide a set of performance specifications that are untatinable with filter-based approaches (25, 26). The use of cDNA clones provides hypridization specificity that is not readily attained with oligoparticular to a capacity of the capacity of the capacity of the pridization specificity that is not readily attained with oligonucleotide arrays (27-30). The parallel format of the assay provides a simultaneous differential expression readout for >1000 genes. This contrasts with sequencing-based methods, which require serial data collection for expression analysis (31. 32). A commercial source of cDNA microarrays would greatly

speed the use of a chip-based approach to expression analysis. The availability of large numbers of ESTs (3) provides a rich resource of human cDNA clones for microarraying. The >400,000 ESTs in the public data bases represent a significant subset of all human genes (3, 33). Microarrays of thousands of ESTs will provide a powerful analytical tool for future human gene expression studies. The -100,000 genes in the human genome (2, 33) emphasize the need for microarrays of greater density. Attempts to improve microdeposition techniques are underway and should allow construction of arrays containing a complete set of human gene targets (http://cmgm.stanford. edu/~schena/). Microarrays of ~100,000 cDNA elements would allow expression monitoring of the entire human genome in a single hybridization. This capacity, coupled with detailed biochemical analysis of the individual gene products. would greatly speed the functional analysis of the human genome

We thank S. Elledge (selledge@bcm.tmc.edu) for the human cDNA library, Qiagen representatives for help with plasmid purification, and A. J. Smith and colleagues at the Protein and Nucleic Acid (PAN) facility (Stanford) for oligonucleotide synthesis and DNA sequencing. We also thank members of the Davis, Brown, and Smith laboratories for critical comments and helpful discussions and Synteni employees for technical assistance. Support for R.W.D. was provided by the National Science Foundation (MCB9106011) and National Institutes of Health (R37HG00198) and for P.O.B. by the National Institutes of Health (3R21HG00450) and Howard Hughes Medical Institute. P.O.B. is an assistant investigator of the Howard Hughes Medical

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> 36 October 1975 Vol. 275 - Pages 349-1

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BOXESTANDE STREETS TO

The Genome Project adds a new dimension to questions on gene expression in humans and model systems. A chart on page 415 summarizes progress in the Caenorhabditis elegans Genome Project and indicates some ways information about sequences can be used.

News stories. Articles. Perspectives, Policy Forums, and Reports focus on technological developments, clinical applications, and ethical concerns resulting from the burgeoning of genomic information, IC. elegans image: F. Maduro and D. Pilgrim, University of Albertal



# REPORTS MARKET TO THE PARTY OF THE PARTY OF

Cosmogenic Ages for Earthquake Recurrence Intervals and Debris Flow Fan Deposition, Owens Valley, California P. R. Bierman, A. R. Gillespie, M. W. Caffee

Lithoautotrophic Microbial 450

Ecosystems in Deep Basalt Aquifers T. O. Stevens and I. P. McKinley

Large Arctic Temperature Change at the Wisconsin-Holocene Glacial Transition K. M. Cuffey, G. D. Clow, R. B. Alley, M. Stuiver,

Superplasticity in Earth's Lower Mantle: 458 Evidence from Seismic Anisotropy and Rock Physics

S.-i. Karato, S. Zhang, H.-R. Wenk Large-Scale Interplanetary Magnetic Field Configuration Revealed by Solar

E. D. Waddington, R. W. Saltus

Radio Bursts M. J. Reiner, J. Fainberg, R. G. Stone Role of Yeast Insulin-Degrading Enzyme 464 Homologs in Propheromone Processing and **Bud Site Selection** 

N. Adames, K. Blundell, M. N. Ashby, C. Boone

Quantitative Monitoring of Gene Expression Patterns with a Complementary DNA Microarray

M. Schena, D. Shalon, R. W. Davis, P. O. Brown

Gene Therapy in Peripheral Blood Lymphocytes and Bone Marrow for ADA Immunodeficient Patients

C. Bordignon, L. D. Notarangelo, N. Nobili, G. Ferrari, G. Casorati, P. Panina, E. Mazzolari, D. Maggioni, C. Rossi, P. Servida, A. G. Ugazio, F. Mavilio

T Lymphocyte-Directed Gene Therapy for ADA SCID: Initial Trial Results After 4 Years

R. M. Blaese, K. W. Culver, A. D. Miller, C. S. Carter, T. Fleisher, M. Clerici, G. Shearer, L. Chang, Y. Chiang, P. Tolstoshev, J. J. Greenblatt, S. A. Rosenberg, H. Klein, M. Berger, C. A. Mullen, W. J. Ramsey, L. Muul, R. A. Morgan, W. F. Anderson

Physical Map and Organization of Arabidopsis thaliana Chromosome 4 R. Schmidt, J. West, K. Love. Z. Lenehan, C. Lister, H. Thompson, D. Bouchez, C. Dean

Serial Analysis of Gene Expression V. E. Velculescu, L. Zhang, B. Vogelstein, K. W. Kinzler

480

# TECHNICAL COMMENTS WINDOWS

The Radius of Gyration of an 487 Apomyoglobin Folding Intermediate D. Eliezer, P. A. Jennings, P. E. Wright, S. Doniach,



Good things in small genomes

AAAS Board of Directors Indicates accompanying feature

461

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K. O. Hodgson, H. Tsuruta

Axito sequence following Ser<sup>208</sup> and occurs within the domain of Axi1p that shows homology with hIDE (14). To delete the complete STE23 sequence and create the ste234::URA3 mutation, polymerase chain reaction (PCR) primers (5'-TCGGAAGACCTCAT-TCTTGCTCATTTTGATATTGCTC- TGTAGATTG-TACTGAGAGTGCAC-3": and 5"-GCTACAAACAGC GTCGACTTGAATGCCCCGACATCTTCGACTGT-GCGGTATTTCACACCG-3') were used to amplify the URA3 sequence of pRS316, and the reaction product was transformed into yeast for one-step gene replacement [R. Rothsten, Methods Enzymol. 194. 281 (1991)]. To create the ax1 A:: LEU2 mutation contained on p114, a 5.0-kb Sal I fragment from pAXL1 was cloned into pUC19, and an internal 4.0-lib Hpa i-Xho I fragment was replaced with a LEU2 fragment. To construct the ste234::LEU2 aliele (a deletion corresponding to 931 amino acids) carned on p153, a LEU2 fragment was used to replace the 2.8-kb Pml I-Ed136 II fragment of STE23, which occurs within a 6.2-kb Hind III-Bgl II genomic fragment carried on pSP72 (Promega). To create YEpMFA1, a 1.6-kb Barn Hi fragment containing MFA1, from pKK16 [K. Kuchler, R. E. Sterne, J. Thorner, EMBO J. 8, 3973 (1989)), was ligated into the Barn HI site of YEp351 [J. E. Hill, A. M. Myers, T. J. Koerner, A. Tzagoloff, Yeast 2 163 (1986)

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- 29. Single-letter abbreviations for the arrino acid re-
- dues are as follows: A. Ala; C. Cys; D. Asp; E. Glu; F. Phe; G, Gly; H, Hs; I, Ile; K, Lys; L, Leu; M, Met; N, Asn; P, Pro; Q, Gh; R, Arg; S, Ser; T, Thr; V, Val; W, Trp: and Y, Tyr.
- A W303 1A derivative, SY2625 (MATa ura3-1 leu2-3, 112 trp1-1 ade2-1 can1-100 sst1 \( \text{mla2} \( \text{L} \):FUS1- lac2 his3A::FUS1-HIS3), was the parent strain for the mutant search. SY2625 derivatives for the mating assays, secreted pheromone assays, and the pulse-chase exper creted pheromone assays, and the pulse-chase experiments included the following strains: Y49 (ste22-1), Y115 [wind hat:LEU2], Y142 [axt1::URA3], Y173 [axt1::LEU2], Y220 [axt1::URA3 ste23a::URA3], Y221 (ste23A::URA3), Y231 (axl1A::LEU2 ste23A::LEU2) and Y233 (ste234::LEU2). MATa derivatives of SYSSES included the following strains: Y199 (SYSES made MATa), Y278 (ste22-1), Y195 (mta14::LEUZ), Y196 (axt14::LEUZ), and Y197 (axt1::LURA3). The EG123 (MATa leu2 ura3 trp1 can1 his4) genetic background was used to create a set of strains for analysis of bud site selection. EG123 destrains for analysis of bud site selection. ECLL 3 de-matives included the following strains: Y175 (ax11a::LEUZ), Y223 (ax11::URA3), Y234 (ste23a:: LEUZ), and Y272 (ax11a::LEUZ ste23a::LEUZ), MATa derivatives of EG123 included the following strains: Y214 (EG123 made MATa) and Y293 (axl1 A::LEU2). All strains were generated by means of standard genetic or molecular methods involving the appropriate constructs (23). In particular, the axi i ste23 double mutant strains were created by crossing of the appropriate MATa ste23 and MATa axif mutants, followed by sporulation of the resultant diploid and isolation of the double mutant from nonparental di-type tetrads. Gene disruptions were confirmed with either PCR or Southern (DNA) analysis.
- 31, p129 is a YEp352 U. E. HB, A. M. Myers, T. J. Koerner, A. Tzagoloff, Yeast 2, 163 (1986)] plasmid containing a 5.5-kb Sal I fragment of pAXL1, p151 was derived from p129 by insertion of a linker at the Bgl II site within AXL1, which led to an in-frame insertio the hemagglutinin (HA) epitope (DOYPYDVPDYA) (29) between amino acids 854 and 855 of the AXL1 prod-

uct, pC225 is a KS+ (Stratagene) plasmid containing a 0.5-kb Barn HI-Sst I tragment from pAXL1. Substitution mutations of the proposed active site of Axin were created with the use of pC225 and site-specific mutagenesis involving appropriate synthetic oligonu-cleotides (aut1-H68A, 5'-GTGCTCACAAAGCGCT-GCCAAACCGGC-3": BUT-E71A, 5"-AAGAATCAT-GTGCGCACAAAGGTGCGC-3": and ax1+E71D. 5"-AAGAATCATGTGATCACAAAGGTGCGC-3"). mutations were confirmed by sequence analysis. After mutagenesis, the 0.4-kb Barn Hi-Msc I fragment from the mutagenized pC225 plasmids was trans-ferred into pAXL1 to create a set of pRS316 plasmids carrying different AXL1 alleles, p124 (ax11-H68A). p130 (ax1-E71A), and p132 (ax1-E71D). Similarly, a set of HA-tagged alleles carried on YEp352 were created after replacement of the p151 Barn Hi-Msc tragment, to generate p161 (axd1-E71A), p162 (axd1H68A), and p163 (axd1-E71D).

32. We thank J. Becker and S. Michaelis for providing a-factor antibodies; S. Michaelis for discussing un published results and helping with the pulse-chase experiments; J. Brown, J. Chant, and S. Sanders for their input concerning bud site selection experiments; M. Raymond, F. Tarminoi, and M. Whiteway for plasmids; M. Marra for providing the STE23 genomic fragment; and H. Bussey, J. Brown, N. Davis, T. Favero, C. de Hoog, and S. Kim for comments on the manuscript. Supported by a grant to C.B. from the Natural Sciences and Engiing Research Council of Canada. Support for M.N.A. was from a California Tobacco-Related Disease Research Program postdoctoral fellowship

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# Quantitative Monitoring of Gene Expression Patterns with a Complementary DNA Microarray

Mark Schena,\* Dari Shalon,\*† Ronald W. Davis. Patrick O. Brown‡

A high-capacity system was developed to monitor the expression of many genes in parallel. Microarrays prepared by high-speed robotic printing of complementary DNAs on glass were used for quantitative expression measurements of the corresponding genes. Because of the small format and high density of the arrays, hybridization volumes of 2 microliters could be used that enabled detection of rare transcripts in probe mixtures derived from 2 micrograms of total cellular messenger RNA. Differential expression measurements of 45 Arabidopsis genes were made by means of simultaneous, two-color fluorescence hybridization.

The temporal, developmental, topographical, histological, and physiological patterns in which a gene is expressed provide clues to its biological role. The large and expanding database of complementary DNA (cDNA) sequences from many organisms (1) presents the opportunity of defining these patterns at the level of the whole genome.

For these studies, we used the small flowering plant Arabidopsis thaliana as a model organism. Arabidopsis possesses many advantages for gene expression analysis, including the fact that it has the smallest genome of any higher eukaryote examined to date (2). Forty-five cloned Arabidopsis cDNAs (Table 1), including 14 complete sequences and 31 expressed sequence tags (ESTs), were used as gene-specific targets. We obtained the ESTs by selecting cDNA clones at random from an Arabidopsis cDNA library. Sequence analysis revealed that 28 of the 31 ESTs matched sequences

in the database (Table 1). Three additional cDNAs from other organisms served as controls in the experiments.

The 48 cDNAs, averaging ~1.0 kb, were amplified with the polymerase chain reaction (PCR) and deposited into individual wells of a 96-well microtiter plate. Each sample was duplicated in two adjacent wells to allow the reproducibility of the arraying and hybridization process to be tested. Samples from the microtiter plate were printed onto glass microscope slides in an area measuring 3.5 mm by 5.5 mm with the use of a high-speed arraying machine (3). The arrays were processed by chemical and heat treatment to attach the DNA sequences to the glass surface and denature them (3). Three arrays, printed in a single lot, were used for the experiments here. A single microtiter plate of PCR products provides sufficient material to print at least 500 arrays.

Fluorescent probes were prepared from total Arabidopsis mRNA (4) by a single round of reverse transcription (5). The Arabidopsis mRNA was supplemented with human acetylcholine receptor (AChR) mRNA at a dilution of 1:10,000 (w/w) before cDNA synthesis, to provide an internal standard for calibration (5). The resulting fluorescently labeled cDNA mixture was hybridized to an array at high stringency (6) and scanned

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with a laser (3). A high-sensitivity scan gave signals that saturated the detector at nearly all of the Arabidopsis target sites (Fig. 1A). Calibration relative to the AChR mRNA standard (Fig. 1A) established a sensitivity limit of ~1:50,000. No detectable hybridization was observed to either the rat glucocorticoid receptor (Fig. 1A) or the yeast TRP4 (Fig. 1A) targets even at the highest scanning sensitivity. A moderate-sensitivity scan of the same army allowed linear detection of the more abundant transcripts (Fig. 1B). Quantitation of both scans revealed a range of expression levels spanning three orders of magnitude for the 45 genes tested (Table 2). RNA blots (7) for several genes (Fig. 2) cornoborated the expression levels measured with the microarray to within a factor of 5 (Table 2).

Differential gene expression was investi-

gated with a simultaneous, two-color hybridization scheme, which served to minmize experimental variation inherent in the comparison of independent hybridizations. Fluorescent probes were prepared from two mRNA sources with the use of reverse transcriptase in the presence of fluorescein- and lissamine-labeled nucleotide analogs, respectively (5). The two probes were then mixed together in equal proportions, hybridized to a single array, and scanned separately for fluorescein and lissamine emission after independent excitation of the two fluorophores (3). To test whether overexpression of a sin-

gle gene could be detected in a pool of total Arabidopsis mRNA, we used a microarray to analyze a transgenic line overexpressing the single transcription factor HAT4 (8). Fluorescent probes representing mRNA from wild-type and HAT4-transgenic plants were labeled with fluorescein and lissamine, respectively; the two probes were then mixed and hybridized to a single array. An intense hybridization signal was observed at the position of the HAT4 cDNA in the lissamine-specific scan (Fig. 1D), but not in the fluorescein-specific scan of the same array (Fig. 1C). Calibration with AChR mRNA added to the fluorescein and lissamine cDNA synthesis reactions at dilutions of 1:10,000 (Fig. 1C) and 1:100 (Fig. 1D). respectively, revealed a 50-fold elevation of HAT4 mRNA in the transgenic line relative to its abundance in wild-type plants (Table 2). This magnitude of HAT4 overexpression matched that inferred from the Northern (RNA) analysis within a factor of 2 (Fig. 2 and Table 2). Expression of all the other genes monitored on the array differed by less than a factor of 5 between HAT4transgenic and wild-type plants (Fig 1, C

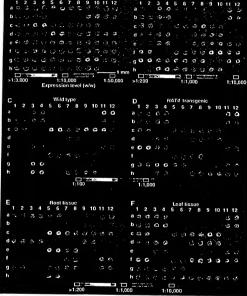


Fig. 1. Gene expression monitored with the use of DNA microarrays. Fluorescent scans represented in pseudocolor correspond to hybridization intensities. Color bars were calibrated from the signal dotained with the use of known concentrations of human ACHR mRNA in independent experiments. Numbers and letters on the axes mark the position of each cDNA. (A) High-sensitivity fluorescen scan after hybridization with fluoresceni-labeled cDNA derived from with-type plants. (B) Same array as in (A) but scanned at most experimental sensitivity. (I and D) A single array was probed with a 1:1 mixture of fluoresceni-labeled cDNA from widd-type plants and issamine-labeled cDNA from HATA-transgenic plants. The single array was then scanned successively to detect the fluorescen fluorescence corresponding to mRNA from MATA-type plants (C) and the issamine fluorescence corresponding to mRNA from ACHA-transgenic plants (C) and the issamine-fluorescence doNA from leaf tissue. The single array was the scanned successively to detect the fluoresceni fluorescenic fluorescence corresponding to mRNAs expressed in roots (E) and the issamine fluorescence corresponding to mRNAs expressed in roots (E) and the issamine fluorescence corresponding to mRNAs expressed in leaves (F).

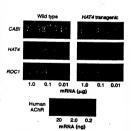


Fig. 2. Gene expression monitored with RNA (Northern) blot analysis. Designated amounts of mRNA from wild-type and HAT4-transperic plants were spotted onto nylon membranes and probed with the cDNAs indicated. Purified human ACRR mRNA was used for calibration.

and D, and Table 2). Hybridization of fluorescein-labeled glucocorticoid receptor CDNA (Fig. IC) and lissamine-labeled TRP4 cDNA (Fig. 1D) verified the preence of the negative control targets and the lack of optical cross talk between the two fluorophores.

To explore a more complex alteration in expression patterns, we performed a second row-color hybridisation experiment with fluorescein- and lissamine-labeled probes prepared from root and leaf mRNA, respectively. The scanning sensitivities for the two fluorophores were normalized by matching the signals resulting from ACAR

mRNA, which was added to both cDNA synthesis reactions at a dilution of 1:1000 (Fig. 1, E and F). A comparison of the scars revealed widespread differences in gene expression between root and leaf tissue (Fig. 1, E and F). The mRNA from the light-regulated CABI gene was ~500-fold more abundant in leaf (Fig. 1F) than in root tissue (Fig. 1E). The expression of 26 other genes differed between root and leaf tissue by more than a factor of 5 (Fig. 1, E and F).

The HAT4-transgenic line we examined has elongated hypocotyls, early flowering, poor germination, and altered pigmentation (8). Although changes in expression were

Table 1. Sequences contained on the cDNA microarray, Shown is the position, the known or putative function, and the accession number of each cDNA in the microarray (Fig. 1). All but three of the ESTs used in this study matched a sequence in the database. NADH, reduced form of nicotramide adenine dinucleotice, ATDses, adenosine triphosphates.

| Position        | cDNA   | Function                      | Accession<br>number |
|-----------------|--------|-------------------------------|---------------------|
| a1, 2           | AChR   | Human AChR                    | •                   |
| 11, 2           | EST3   | Actin                         | H36236              |
| 15. 6           | EST6   | NADH dehydrogenase            | Z27010              |
|                 | AAC1   | Actin 1                       | M20016              |
| 7, 8            | EST12  | Unknown                       | U36594†             |
| 9, 10           | EST13  | Actin                         | T45783              |
| 11, 12          | CABI   | Chlorophyll a/b binding       | M85150              |
| 1, 2            | EST17  | Phosphoglycerate kinase       | T44490              |
| 3. 4            | GA4    | Gibberellic acid biosynthesis | L37126              |
| 5, 6            | EST19  | Unknown                       | U36595†             |
| o7, B           |        | G-box binding factor 1        | x63894              |
| 9, 10           | GBF-1  | Elongation factor             | X52256              |
| 11, 12          | EST23  | Aldolase                      | T04477              |
| 1, 2            | EST29  | G-box binding factor 2        | X63895              |
| :3, 4           | GBF-2  |                               | R87034              |
| :5, 6           | EST34  | Chloroplast protease          | T14152              |
| 7, 8            | EST35  | Unknown                       | T22720              |
| 9, 10           | EST41  | Catalase                      | M14053              |
| 11, 12          | rGR    | Rat glucocorticoid receptor   |                     |
| 11. 2           | EST42  | Unknown                       | U36596              |
| 13, 4           | EST45  | ATPase                        | J04185              |
| 15. 6           | HAT1   | Homeobox-leucine zipper 1     | U09332              |
| 17. 8           | EST46  | Light harvesting complex      | T04063              |
| 19. 10          | EST49  | Unknown                       | T76267              |
| 111, 12         | HAT2   | Homeobox-leucine zipper 2     | U09335              |
| 1.2             | HAT4   | Homeobox-leucine zipper 4     | M90394              |
| 3. 4            | EST50  | Phosphoribulokinase           | T04344              |
| e5. 6           | HAT5   | Homeobox-leucine zipper 5     | M90416              |
| 27. 8           | EST51  | Unknown                       | Z33675              |
| 9. 10           | HAT22  | Homeobox-leucine zipper 22    | U09336              |
| 911, 12         | EST52  | Oxygen evolving               | T21749              |
|                 | EST59  | Unknown                       | Z34607              |
| 11, 2           | KNAT1  | Knotted-like homeobox 1       | U14174              |
| 13. 4           | EST60  | RuBisCO small subunit         | X14564              |
| 15. 6           | EST69  | Translation elongation factor | T42799              |
| 7,8             |        | Protein phosphatase 1         | U34803              |
| 9, 10           | PPH1   | Unknown                       | T44621              |
| f11, <b>1</b> 2 | EST70  | Chloroplast protease          | T43698              |
| g1, 2           | EST75  |                               | R65481              |
| g3, 4           | EST78  | Unknown                       | L14844              |
| g5, 6           | ROC1   | Cyclophilin                   | X59152              |
| g7, 8           | EST82  | GTP binding                   | Z33795              |
| g9, 10          | EST83  | Unknown                       |                     |
| g11, 12         | EST84  | Unknown                       | T45278<br>T13832    |
| h1, 2           | EST91  | Unknown                       |                     |
| h3, 4           | EST96  | Unknown                       | R64816              |
| h5, 6           | SAR1   | Synaptobrevin                 | M9041               |
| h7. 8           | EST100 | Light harvesting complex      | Z18205              |
| h9. 10          | EST103 | Light harvesting complex      | X03909              |
| h11, 12         | TRP4   | Yeast tryptophan biosynthesis | X04273              |

observed for HAT4, large changes in expression were not observed for any of the other 44 genes we examined. This was somewhat surprising, particularly because comparative analysis of leaf and root tissue identified 27 differentially expressed genes. Analysis of an expanded set of genes may be required to identify genes whose expression changes upon HAT4 overexpression; alternatively, a comparison of mRNAa populations from specific tissues of wild-type and HAT4-transgenic plants may allow identification of downstream genes.

At the current density of robotic printing, it is feasible to scale up the fabrication process to produce arrays containing 20,000 cDNA targets. At this density, a single array would be sufficient to provide gene-specific targets encompassing nearly the entire reperioric of expressed genes in the Arabidopsis genome (2). The availability of 20,274 ESTs from Arabidopsis (1, 9) would provide a rich source of remolates for such studies.

The estimated 100,000 genes in the human genome (10) exceeds the number of Arabidopsis genes by a factor of 5 (2). This modest increase in complexity suggests that similar cDNA microarrays, prepared from the rapidly growing repertoire of human ESTs (1), could be used to determine the expression parterns of tens of thousands of human genes in diverse cell types. Coupling an amplification strategy to the reverse transcription reaction (11) could make it feasible to monitor expression even in minute tissue samples. A wide variety of acute and chronic physiological and pathological conditions might lead to characteristic changes in the patterns of gene expression in peripheral blood cells or other easily sampled tissues. In concert with cDNA microarrays for monitoring complex expression patterns, these tissues might therefore serve as sensitive in vivo sensors for clinical diagnosis. Microarrays of cDNAs could thus provide a useful link between human gene sequences and clinical medicine.

Table 2. Gene expression monitoring by microarray and RNA bolt analyses; i.g. MAT4-transgenic. See Table 1 for additional gene information. Expression levels (w/w) were cabbrated with the use of lenown amounts of human ACNR mRNA. Values for the microarray were determined from microarray scans (Fig. 1); values for the RNA blot were determined from RNA blots (Fig. 2).

| _         | Expression | level (w/w) |  |
|-----------|------------|-------------|--|
| Gene      | Microarray | RNA blot    |  |
| CABI      | 1:48       | 1:83        |  |
| CABI (tg) | 1:120      | 1:150       |  |
| HAT4      | 1:8300     | 1:6300      |  |
| HAT4 (tg) | 1:150      | 1:210       |  |
| ROC1      | 1:1200     | 1:1800      |  |
| ROC1 (tq) | 1:260      | 1:1300      |  |

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D. Shalon, thesis, Stanford University (1995); \_\_\_\_\_\_ and P. O. Brown, in preparation. Microarrays were fabricated on poly-L-lysine-coated microscope slides (Sigma) with a custom-built arraying machine fitted with one printing tip. The tip loaded 1 µl of PCR product (0.5 mg/ml) from 96-well microtiter plate and deposited ~0.005 µl per side on 40 sides at a spacing of 500 um. The printed slides were rehydrated for 2 hours in a humid chamber, snap-dned at 100°C for 1 min, rinsed in 0.1% SDS, and treated with 0.05% succinic anhydride prepared in buffer consisting of 50% 1-methyl-2-pyrrolidinone and 50% boric acid. The cDNA on the sides was denatured in distilled water for 2 min at 90°C immediately before use. Microarrays were scanned with a lase fluorescent scanner that contained a computer-controlled XY stage and a microscope objective. A mixed gas, multiline laser allowed sequential excitation of the two fluorophores. Emitted light was split according to wavelength and detected with two photomu tiplier tubes. Signals were read into a PC with the use of a 12-bit analog-to-digital board. Additional details of microarray fabrication and use may be obtained by means of e-mail (pbrown@cmgm. stanford.edu). F. M. Ausubel et al., Eds., Current Protocols in Mo-

lecutar Biology (Greene & Wiley Interscience, New

York, 1994), pp. 4.3.1-4.3.4. Polyadenylated [poly(A)\*] mRNA was prepared from total RNA with the use of Oligotex-dT resin (Qiagen). Reverse transcription (RT) rea ith a StrataScript RT-PCR kit (Stratagene) modified as follows: 50-µl reactions contained 0.1 µg/µl of Arabidopsis mRNA, 0.1 ng/µl of human AChR mRNA, 0.05 μg/μl of oligo(dT) (21-mer), 1× first strand buffer, 0.03 U/μl of ribonuclease block, 500 μM deoxyadenosine triphosphate (dATP), 500 μM oxyguanosine triphosphate, 500 µM dTTP, 40 μM deoxycytosine triphosphate (dCTP), 40 μM fluorescein-12-dCTP for Essamine-5-dCTP1 and 0.03 I Visit of Strata Script reverse transcriptage Reactions were incubated for 60 min at 37°C, precipitated with ethanol, and resuspended in 10 µl of TE (10 mM tris-HCI and 1 mM EDTA, pH 8.0). Samples were then heated for 3 min at 94°C and chilled on ice. The RNA was degraded by adding 0.25 µJ of 10 N NaOH followed by a 10-min incubation at 37°C. The samples were neutralized by addition of 2.5 µl of 1 M tns-Cl (pH 8.0) and 0.25 µl of 10 N HCl and precipitated with ethanol. Peliets were washed with 70% ethanol, dried to completion in a speedvac, resuspended in 10 µl of H2O, and reduced to 3.0 µl in a speedvac. Fluorescent nucleotide analogs were ob-tained from New England Nuclear (DuPont).

Hybridization reactions contained 1.0 µJ of fluorescent cDNA synthesis product (5) and 1.0 µJ of hybridization buffer [10× saine sodium citrate (SSC) and 0.2% SDS). The 2 Day I nonhe mint yes were aliculated anto the microarray surface and covered with cover stips (12 mm round). Arrays were transferred to a hybridization chamber (3) and incubated for 18 hours at 65°C. Arrays were washed for 5 min at room temperature (25°C) in low-stringency wash buffer (1× SSC and 0.1% SDS), then for 10 min at room temperature in high-stringency wash buffer (0.1 × SSC and 0.1% SDS). Arrays were scanned in 0.1× SSC with the use of a fluorescence laser-scanning device (3).

Samples of poly(A)\* mRNA (4, 5) were spotted onto nylon membranes (Nytran) and crosslinked with uftraviolet light with the use of a Stratalinker 1800 (Stratagene). Probes were prepared by random priming with the use of a Prime-It II kit (Stratagene) in the presence of P2PIdATP, Hybridizations were carned out according to the instructions of the manufacturer. Quantitation was performed on a Phos-

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12. The laser fluorescent scanner was designed and tabncated in collaboration with S. Smith of Stanford University. Scanner and analysis software was developed by R. X. Xia. The succinic anhydroge reaction was a mose: ed by J. Mulligan and J. Van Ness of Darwn Molecular Corporation, Thanks to S. Theologs, C. Somerville, K. Yamamoto, and members of the laboratones of R.W.D. and P.O.B. for critical comments. Supported by the Howard Hughes Medical Institute and by grants from NiH [R21HG00450] (P.O.B.) and R37AG00198 (R.W.D.)) and from NSF (MCB9106011) (R.W.D.) and by an NSF graduate fellowship (D.S.). P.O.B. is an assistant investigator of the Howard Hughes Medical

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# Gene Therapy in Peripheral Blood Lymphocytes and Bone Marrow for ADA Immunodeficient Patients

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Adenosine deaminase (ADA) deficiency results in severe combined immunodeficiency. the first genetic disorder treated by gene therapy. Two different retroviral vectors were used to transfer ex vivo the human ADA minigene into bone marrow cells and peripheral blood lymphocytes from two patients undergoing exogenous enzyme replacement therapy. After 2 years of treatment, long-term survival of T and B lymphocytes, marrow cells. and granulocytes expressing the transferred ADA gene was demonstrated and resulted in normalization of the immune repertoire and restoration of cellular and humoral immunity. After discontinuation of treatment, T lymphocytes, derived from transduced peripheral blood lymphocytes, were progressively replaced by marrow-derived T cells in both patients. These results indicate successful gene transfer into long-lasting progenitor cells, producing a functional multilineage progeny.

Severe combined immunodeficiency associated with inherited deficiency of ADA (1) is usually fatal unless affected children are kept in protective isolation or the immune system is reconstituted by bone marrow transplantation from a human leukocyte antigen (HLA)-identical sibling donor (2). This is the therapy of choice, although it is available only for a minority of patients. In recent years, other forms of therapy have been developed, including transplants from haploidentical donors (3, 4), exogenous enzyme replacement (5), and somatic-cell gene therapy (6-9).

We previously reported a preclinical model in which ADA gene transfer and expression

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successfully restored immune functions in human ADA-deficient (ADA-) peripheral blood lymphocytes (PBLs) in immunodeficient mice in vivo (10, 11). On the basis of these preclinical results, the clinical application of gene therapy for the treatment of ADA - SCID (severe combined immunodeficiency disease) patients who previously failed exogenous enzyme replacement therapy was approved by our Institutional Ethical Committees and by the Italian National Committee for Bioethics (12). In addition to evaluating the safety and efficacy of the gene therapy procedure, the aim of the study was to define the relative role of PBLs and hematopoietic stem cells in the long-term reconstitution of immune functions after retroviral vector-mediated ADA gene transfer. For this purpose, two structurally identical vectors expressing the human ADA complementary DNA (cDNA), distinguishable by the presence of alternative restriction sites in a nonfunctional region of the viral long-terminal repeat (LTR), were used to transduce PBLs and bone marrow (BM) cells independently. This procedure allowed identification of the origin of

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| (54) Title: METHOD AND APPARATUS FOR FABRIC  | ATING            | MICROARRAYS OF BIOLOGICAL SAMPLES                                |  |  |
| (57) Abstract  |                  |  |  |  |
| (37) Abstract<br>A method and apparatus for forming microarrays of biological samples on a support are disclosed. The method involves dispensing<br>a known volume of a reagent at each of a selected array position, by tapping a capillary dispenser on the support under conditions effective<br>to draw a defined volume of liquid onto the support. The apparatus is designed to produce a microarray of such regions in an automated<br>fashion. |                  |  |  |  |
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WO 95/35505 PCT/US95/07659

#### METEOD AND APPARATUS FOR FABRICATING MICROARRAYS OF BIOLOGICAL SAMPLES

#### Field of the Invention

This invention relates to a method and apparatus for fabricating microarrays of biological samples for large scale screening assays, such as arrays of DNA samples to be used in DNA hybridization assays for genetic research and diagnostic applications.

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# Background of the Invention

A variety of methods are currently available for making arrays of biological macromolecules, such as arrays of nucleic acid molecules or proteins. One method for making ordered arrays of DNA on a porous membrane is a "dot blot" approach. In this method, a vacuum manifold transfers a plurality, e.g., 96, aqueous samples of DNA from 3 millimeter diameter wells to a porous membrane. A common variant of this procedure is a "slot-blot" method in which the wells have highly-elongated oval shapes.

The DNA is immobilized on the porous membrane by baking the membrane or exposing it to UV radiation. This is a manual procedure practical for making one array at a time and usually limited to 96 samples per array. "Dot-blot" procedures are therefore inadequate for applications in which many thousand samples must be determined.

25 A more efficient technique employed for making ordered arrays of genomic fragments uses an array of pins dipped into the wells, e.g., the 96 wells of a microtitre plate, for transferring an array of samples to a substrate, such as a porous membrane. One array includes pins that are designed to spot a membrane in a staggered fashion, for creating an array of 9216 spots in a 22 × 22 cm area (Lehrach, et al., 1990). A limitation with this approach is that the volume of DNA spotted in each pixel of each array is highly variable.

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In addition, the number of arrays that can be made with each dipping is usually guite small.

An alternate method of creating ordered arrays of nucleic acid sequences is described by Firrung, et al.

5 (1992), and also by Fodor, et al. (1991). The method involves synthesizing different nucleic acid sequences at different discrete regions of a support. This method employs elaborate synthetic schemes, and is generally limited to relatively short nucleic acid

10 sample, e.g., less than 20 bases. A related method has been described by Southern. et al. (1992).

Khrapko, et al. (1991) describes a method of making an oligonuclectide matrix by spotting DNA onto a thin layer of polyacrylamide. The spotting is done manually with a micropicette.

None of the methods or devices described in the prior art are designed for mass fabrication of microarrays characterized by (i) a large number of micro-sized assay regions separated by a distance of 50-200 microns or less, and (ii) a well-defined amount, typically in the picomole range, of analyte associated with each region of the array.

Furthermore, current technology is directed at performing such assays one at a time to a single array of DNA molecules. For example, the most common method for performing DNA hybridizations to arrays spotted onto porous membrane involves sealing the membrane in a plastic bag (Maniatas, et al., 1989) or a rotating glass cylinder (Robbins Scientific) with the labeled hybridization probe inside the sealed chamber. For arrays made on non-porous surfaces, such as a microscope slide, each array is incubated with the labeled hybridization probe sealed under a coverslip. These techniques require a separate sealed chamber for

each array which makes the screening and handling of many such arrays inconvenient and time intensive.

Abouzied, et al. (1994) describes a method of printing horizontal lines of antibodies on a 5 nitrocellulose membrane and separating regions of the membrane with vertical stripes of a hydrophobic material. Each vertical stripe is then reacted with a different antigen and the reaction between the immobilized antibody and an antigen is detected using a 10 standard ELISA colorimetric technique. Abouzied's technique makes it possible to screen many onedimensional arrays simultaneously on a single sheet of nitrocellulose. Abouzied makes the nitrocellulose somewhat hydrophobic using a line drawn with PAP Pen 15 (Research Products International). However Abouzied does not describe a technology that is capable of completely sealing the pores of the nitrocellulose. The pores of the nitrocellulose are still physically open and so the assay reagents can leak through the 20 hydrophobic barrier during extended high temperature incubations or in the presence of detergents which makes the Abouzied technique unacceptable for DNA hybridization assays.

Porous membranes with printed patterns of

hydrophilic/hydrophobic regions exist for applications
such as ordered arrays of bacteria colonies. QA Life
Sciences (San Diego CA) makes such a membrane with a
grid pattern printed on it. However, this membrane has
the same disadvantage as the Abouzied technique since
reagents can still flow between the gridded arrays
making them unusable for separate DNA hybridization
assays.

Pall Corporation make a 96-well plate with a porous filter heat sealed to the bottom of the plate.

These plates are capable of containing different

reagents in each well without cross-contamination. However, each well is intended to hold only one target element whereas the invention described here makes a microarray of many biomolecules in each subdivided region of the solid support. Furthermore, the 96 well plates are at least 1 cm thick and prevent the use of the device for many colorimetric, fluorescent and radioactive detection formats which require that the membrane lie flat against the detection surface. The invention described here requires no further processing

invention described here requires no further processing after the assay step since the barriers elements are shallow and do not interfere with the detection step thereby greatly increasing convenience.

Hyseq Corporation has described a method of making
an "array of arrays" on a non-porous solid support for
use with their sequencing by hybridization technique.
The method described by Hyseq involves modifying the
chemistry of the solid support material to form a
hydrophobic grid pattern where each subdivided region
contains a microarray of biomolecules. Hyseq's flat
hydrophobic pattern does not make use of physical
blocking as an additional means of preventing cross

#### 25 Summary of the Invention

contamination.

The invention includes, in one aspect, a method of forming a microarray of analyte-assay regions on a solid support, where each region in the array has a known amount of a selected, analyte-specific reagent.

30 The method involves first loading a solution of a selected analyte-specific reagent in a reagent-dispensing device having an elongate capillary channel (i) formed by spaced-apart, coextensive elongate members, (ii) adapted to hold a quantity of the reagent solution and (iii) having a tip region at which aqueous

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solution in the channel forms a meniscus. The channel is preferably formed by a pair of spaced-apart tapered elements.

The tip of the dispensing device is tapped against
a solid support at a defined position on the support
surface with an impulse effective to break the meniscus
in the capillary channel deposit a selected volume of
solution on the surface, preferably a selected volume
in the range 0.01 to 100 nl. The two steps are
repeated until the desired array is formed.

The method may be practiced in forming a plurality of such arrays, where the solution-depositing step is are applied to a selected position on each of a plurality of solid supports at each repeat cycle.

The dispensing device may be loaded with a new solution, by the steps of (i) dipping the capillary channel of the device in a wash solution, (ii) removing wash solution drawn into the capillary channel, and (iii) dipping the capillary channel into the new reagent solution.

Also included in the invention is an automated apparatus for forming a microarray of analyte-assay regions on a plurality of solid supports, where each region in the array has a known amount of a selected, analyte-specific reagent. The apparatus has a holder for holding, at known positions, a plurality of planar supports, and a reagent dispensing device of the type described above.

The apparatus further includes positioning
structure for positioning the dispensing device at a
selected array position with respect to a support in
said holder, and dispensing structure for moving the
dispensing device into tapping engagement against a
support with a selected impulse effective to deposit a

WO 95/35505

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selected volume on the support, e.g., a selected volume in the volume range 0.01 to 100 nl.

The positioning and dispensing structures are controlled by a control unit in the apparatus. The unit operates to (i) place the dispensing device at a loading station, (ii) move the capillary channel in the device into a selected reagent at the loading station, to load the dispensing device with the reagent, and (iii) dispense the reagent at a defined array position on each of the supports on said holder. The unit may further operate, at the end of a dispensing cycle, to wash the dispensing device by (i) placing the dispensing device at a washing station, (ii) moving the capillary channel in the device into a wash fluid, to load the dispensing device with the fluid, and (iii)

remove the wash fluid prior to loading the dispensing device with a fresh selected reagent.

The dispensing device in the apparatus may be one of a plurality of such devices which are carried on the 20 arm for dispensing different analyte assay reagents at selected spaced array positions.

In another aspect, the invention includes a

substrate with a surface having a microarray of at least 10<sup>3</sup> distinct polynucleotide or polypeptide biopolymers in a surface area of less than about 1 cm<sup>2</sup>. Each distinct biopolymer (i) is disposed at a separate, defined position in said array, (ii) has a length of at least 50 subunits, and (iii) is present in a defined

amount between about 0.1 femtomoles and 100 nanomoles.

In one embodiment, the surface is glass slide surface coated with a polycationic polymer, such as polylysine, and the biopolymers are polynucleotides. In another embodiment, the substrate has a waterimpermeable backing, a water-permeable film formed on

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the backing, and a grid formed on the film. The grid is composed of intersecting water-impervious grid elements extending from said backing to positions raised above the surface of said film, and partitions the film into a plurality of water-impervious cells. A biopolymer array is formed within each well.

More generally, there is provided a substrate for use in detecting binding of labeled polynuclectides to one or more of a plurality different-sequence, immobilized polynuclectides. The substrate includes, in one aspect, a glass support, a coating of a polycationic polymer, such as polylysine, on said surface of the support, and an array of distinct polynuclectides electrostatically bound non-covalently to said coating, where each distinct biopolymer is disposed at a separate, defined position in a surface

array of polynucleotides.

In another aspect, the substrate includes a waterimpermeable backing, a water-permeable film formed on
the backing, and a grid formed on the film, where the
grid is composed of intersecting water-impervious grid
elements extending from the backing to positions raised
above the surface of the film, forming a plurality of
cells. A biopolymer array is formed within each cell.

Also forming part of the invention is a method of detecting differential expression of each of a plurality of genes in a first cell type, with respect to expression of the same genes in a second cell type. In practicing the method, there is first produced fluorescent-labeled cDNA's from mRNA's isolated from

30 fluorescent-labeled cDNA's from mRNA's isolated from the two cells types, where the cDNA's from the first and second cells are labeled with first and second different fluorescent reporters.

A mixture of the labeled cDNA's from the two cell types is added to an array of polynucleotides

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representing a plurality of known genes derived from the two cell types, under conditions that result in hybridization of the cDNA's to complementary-sequence polynucleotides in the array. The array is then examined by fluorescence under fluorescence excitation conditions in which (i) polynucleotides in the array that are hybridized predominantly to cDNA's derived from one of the first and second cell types give a distinct first or second fluorescence emission color, respectively, and (ii) polynucleotides in the array that are hybridized to substantially equal numbers of cDNA's derived from the first and second cell types give a distinct combined fluorescence emission color, respectively. The relative expression of known genes in the two cell types can then be determined by the observed fluorescence emission color of each spot.

These and other objects and features of the invention will become more fully apparent when the following detailed description of the invention is read in conjunction with the accompanying figures.

### Brief Description of the Drawings

Fig. 1 is a side view of a reagent-dispensing device having a open-capillary dispensing head constructed for use in one embodiment of the invention;

Figs. 2A-2C illustrate steps in the delivery of a fixed-volume bead on a hydrophobic surface employing the dispensing head from Fig. 1, in accordance with one embodiment of the method of the invention;

Fig. 3 shows a portion of a two-dimensional array
of analyte-assay regions constructed according to the
method of the invention;

Fig. 4 is a planar view showing components of an automated apparatus for forming arrays in accordance with the invention.

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Fig. 5 shows a fluorescent image of an actual 20  $\times$  20 array of 400 fluorescently-labeled DNA samples immobilized on a poly-1-lysine coated slide, where the total area covered by the 400 element array is 16 square millimeters;

Fig. 6 is a fluorescent image of a 1.8 cm  $\times$  1.8 cm microarray containing lambda clones with yeast inserts, the fluorescent signal arising from the hybridization to the array with approximately half the yeast genome labeled with a green fluorophore and the other half with a red fluorophore:

Fig. 7 shows the translation of the hybridization image of Fig. 6 into a karyotype of the yeast genome, where the elements of Fig.-6 microarray contain yeast DNA sequences that have been previously physically mapped in the yeast genome:

Fig. 8 show a fluorescent image of a 0.5 cm × 0.5 cm microarray of 24 cDNA clones, where the microarray was hybridized simultaneously with total cDNA from wild type Arabidopsis plant labeled with a green fluorophore and total cDNA from a transgenic Arabidopsis plant labeled with a red fluorophore, and the arrow points to the cDNA clone representing the gene introduced into the transgenic Arabidopsis plant;

25 Fig. 9 shows a plan view of substrate having an array of cells formed by barrier elements in the form of a grid;

Fig. 10 shows an enlarged plan view of one of the cells in the substrate in Fig. 9, showing an array of polynucleotide regions in the cell:

Fig. 11 is an enlarged sectional view of the substrate in Fig. 9, taken along a section line in that figure; and

Fig. 12 is a scanned image of a 3 cm × 3 cm 35 nitrocellulose solid support containing four identical

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arrays of M13 clones in each of four quadrants, where each quadrant was hybridized simultaneously to a different oligonucleotide using an open face hybridization method.

Detailed Description of the Invention

#### I. Definitions

Unless indicated otherwise, the terms defined below have the following meanings:

"Ligand" refers to one member of a ligand/antiligand binding pair. The ligand may be, for example, one of the nucleic acid strands in a complementary, hybridized nucleic acid duplex binding pair; an effector molecule in an effector/receptor binding pair; or an antigen in an antigen/antibody or antigen/antibody fragment binding pair.

"Antiligand" refers to the opposite member of a ligand/anti-ligand binding pair. The antiligand may be the other of the nucleic acid strands in a

- 20 complementary, hybridized nucleic acid duplex binding pair; the receptor molecule in an effector/receptor binding pair; or an antibody or antibody fragment molecule in antigen/antibody or antigen/antibody fragment binding pair, respectively.
- 25 "Analyte" or "analyte molecule" refers to a molecule, typically a macromolecule, such as a polynucleotide or polypeptide, whose presence, amount, and/or identity are to be determined. The analyte is one member of a ligand/anti-ligand pair.
- "Analyte-specific assay reagent" refers to a molecule effective to bind specifically to an analyte molecule. The reagent is the opposite member of a ligand/anti-ligand binding pair.

An "array of regions on a solid support" is a 35 linear or two-dimensional array of preferably discrete

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regions, each having a finite area, formed on the surface of a solid support.

A "microarray" is an array of regions having a density of discrete regions of at least about 100/cm², and preferably at least about 1000/cm². The regions in a microarray have typical dimensions, e.g., diameters, in the range of between about 10-250 µm, and are separated from other regions in the array by about the same distance.

A support surface is "hydrophobic" if a aqueousmedium droplet applied to the surface does not spread out substantially beyond the area size of the applied droplet. That is, the surface acts to prevent spreading of the droplet applied to the surface by hydrophobic interaction with the droplet.

A "meniscus" means a concave or convex surface that forms on the bottom of a liquid in a channel as a result of the surface tension of the liquid.

"Distinct biopolymers", as applied to the biopolymers forming a microarray, means an array member which is distinct from other array members on the basis of a different biopolymer sequence, and/or different concentrations of the same or distinct biopolymers, and/or different mixtures of distinct or different-

25 concentration biopolymers. Thus an array of "distinct polynucleotides" means an array containing, as its members, (i) distinct polynucleotides, which may have a defined amount in each member, (ii) different, graded concentrations of given-sequence polynucleotides,

30 and/or (iii) different-composition mixtures of two or more distinct polynucleotides.

"Cell type" means a cell from a given source, e.g., a tissue, or organ, or a cell in a given state of

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differentiation, or a cell associated with a given pathology or genetic makeup.

#### II. Method of Microarray Formation

This section describes a method of forming a microarray of analyte-assay regions on a solid support or substrate, where each region in the array has a known amount of a selected, analyte-specific reagent.

Fig. 1 illustrates, in a partially schematic view, a reagent-dispensing device 10 useful in practicing the method. The device generally includes a reagent dispenser 12 having an elongate open capillary channel 14 adapted to hold a quantity of the reagent solution, such as indicated at 16, as will be described below. The capillary channel is formed by a pair of spacedapart, coextensive, elongate members 12a, 12b which are tapered toward one another and converge at a tip or tip

region 18 at the lower end of the channel. More generally, the open channel is formed by at least two elongate, spaced-apart members adapted to hold a quantity of reagent solutions and having a tip region at which aqueous solution in the channel forms a meniscus, such as the concave meniscus illustrated at 20 in Fig. 2A. The advantages of the open channel

25 construction of the dispenser are discussed below. With continued reference to Fig. 1, the dispenser device also includes structure for moving the dispenser rapidly toward and away from a support surface, for effecting deposition of a known amount of solution in

30 the dispenser on a support, as will be described below with reference to Figs. 2A-2C. In the embodiment shown, this structure includes a solenoid 22 which is activatable to draw a solenoid piston 24 rapidly downwardly, then release the piston, e.g., under spring

35 bias, to a normal, raised position, as shown. The

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dispenser is carried on the piston by a connecting member 26, as shown. The just-described moving structure is also referred to herein as dispensing means for moving the dispenser into engagement with a solid support, for dispensing a known volume of fluid on the support.

The dispensing device just described is carried on an arm 28 that may be moved either linearly or in an xy plane to position the dispenser at a selected deposition position, as will be described.

Figs. 2A-2C illustrate the method of depositing a known amount of reagent solution in the just-described dispenser on the surface of a solid support, such as the support indicated at 30. The support is a polymer, glass, or other solid-material support having a surface indicated at 31.

In one general embodiment, the surface is a relatively hydrophilic, i.e., wettable surface, such as a surface having native, bound or covalently attached charged groups. On such surface described below is a glass surface having an absorbed layer of a polycationic polymer, such as poly-1-lysine.

In another embodiment, the surface has or is formed to have a relatively hydrophobic character,

25 i.e., one that causes aqueous medium deposited on the surface to bead. A variety of known hydrophobic polymers, such as polystyrene, polypropylene, or polyethylene have desired hydrophobic properties, as do glass and a variety of lubricant or other hydrophobic films that may be applied to the support surface.

Initially, the dispenser is loaded with a selected analyte-specific reagent solution, such as by dipping the dispenser tip, after washing, into a solution of the reagent, and allowing filling by capillary flow

35 into the dispenser channel. The dispenser is now moved

to a selected position with respect to a support surface, placing the dispenser tip directly above the support-surface position at which the reagent is to be deposited. This movement takes place with the

dispenser tip in its raised position, as seen in Fig. 2A, where the tip is typically at least several 1-5 mm above the surface of the substrate.

With the dispenser so positioned, solenoid 22 is now activated to cause the dispenser tip to move

10 rapidly toward and away from the substrate surface, making momentary contact with the surface, in effect, tapping the tip of the dispenser against the support surface. The tapping movement of the tip against the surface acts to break the liquid meniscus in the tip channel, bringing the liquid in the tip into contact with the support surface. This, in turn, produces a flowing of the liquid into the capillary space between the tip and the surface, acting to draw liquid out of the dispenser channel, as seen in Fig. 2B.

20 Fig. 2C shows flow of fluid from the tip onto the support surface, which in this case is a hydrophobic surface. The figure illustrates that liquid continues to flow from the dispenser onto the support surface until it forms a liquid bead 32. At a given bead size, 25 i.e., volume, the tendency of liquid to flow onto the surface will be balanced by the hydrophobic surface interaction of the bead with the support surface, which acts to limit the total bead area on the surface, and by the surface tension of the droplet, which tends toward a given bead curvature. At this point, a given 30 bead volume will have formed, and continued contact of the dispenser tip with the bead, as the dispenser tip is being withdrawn, will have little or no effect on

bead volume.

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For liquid-dispensing on a more hydrophilic surface, the liquid will have less of a tendency to bead, and the dispensed volume will be more sensitive to the total dwell time of the dispenser tip in the immediate vicinity of the support surface, e.g., the positions illustrated in Figs. 2B and 2C.

The desired deposition volume, i.e., bead volume, formed by this method is preferably in the range 2 pl (picoliters) to 2 nl (nanoliters), although volumes as 10 high as 100 nl or more may be dispensed. It will be appreciated that the selected dispensed volume will depend on (i) the "footprint" of the dispenser tip, i.e., the size of the area spanned by the tip, (ii) the hydrophobicity of the support surface, and (iii) the 15 time of contact with and rate of withdrawal of the tip from the support surface. In addition, bead size may be reduced by increasing the viscosity of the medium, effectively reducing the flow time of liquid from the dispenser onto the support surface. The drop size may 20 be further constrained by depositing the drop in a hydrophilic region surrounded by a hydrophobic grid

pattern on the support surface.

In a typical embodiment, the dispenser tip is tapped rapidly against the support surface, with a 25 total residence time in contact with the support of less than about 1 msec, and a rate of upward travel from the surface of about 10 cm/sec.

Assuming that the bead that forms on contact with the surface is a hemispherical bead, with a diameter approximately equal to the width of the dispenser tip, as shown in Fig. 2C, the volume of the bead formed in relation to dispenser tip width (d) is given in Table 1 below. As seen, the volume of the bead ranges between 2 pl to 2 nl as the width size is increased from about 20 to 200 um.

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# Table 1

| a      | Volume (nl)            |
|--------|------------------------|
| 20 μm  | 2 × 10 <sup>-3</sup>   |
| 50 μm  | 3.1 × 10 <sup>-2</sup> |
| 100 µm | 2.5 × 10 <sup>-1</sup> |
| 200 μm | 2                      |

At a given tip size, bead volume can be reduced in a controlled fashion by increasing surface hydrophobicity, reducing time of contact of the tip with the surface, increasing rate of movement of the tip away from the surface, and/or increasing the viscosity of the medium. Once these parameters are fixed, a selected deposition volume in the desired pl to nl range can be achieved in a repeatable fashion.

After depositing a bead at one selected location on a support, the tip is typically moved to a corresponding position on a second support, a droplet is deposited at that position, and this process is repeated until a liquid droplet of the reagent has been deposited at a selected position on each of a plurality of supports.

The tip is then washed to remove the reagent liquid, filled with another reagent liquid and this reagent is now deposited at each another array position on each of the supports. In one embodiment, the tip is washed and refilled by the steps of (i) dipping the capillary channel of the device in a wash solution, (ii) removing wash solution drawn into the capillary channel, and (iii) dipping the capillary channel into the new reagent solution.

Prom the foregoing, it will be appreciated that the tweezers-like, open-capillary dispenser tip

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provides the advantages that (i) the open channel of the tip facilitates rapid, efficient washing and drying before reloading the tip with a new reagent, (ii) passive capillary action can load the sample directly from a standard microwell plate while retaining sufficient sample in the open capillary reservoir for the printing of numerous arrays, (iii) open capillaries are less prone to clogging than closed capillaries, and (iv) open capillaries do not require a perfectly faced bottom surface for fluid delivery.

A portion of a microarray 36 formed on the surface 38 of a solid support 40 in accordance with the method just described is shown in Fig. 3. The array is formed of a plurality of analyte-specific reagent regions, such as regions 42, where each region may include a different analyte-specific reagent. As indicated above, the diameter of each region is preferably between about 20-200 µm. The spacing between each region and its closest (non-diagonal) neighbor,

- 20 measured from center-to-center (indicated at 44), is preferably in the range of about 20-400 µm. Thus, for example, an array having a center-to-center spacing of about 250 µm contains about 40 regions/cm or 1,600 regions/cm<sup>2</sup>. After formation of the array, the support
- 25 is treated to evaporate the liquid of the droplet forming each region, to leave a desired array of dried, relatively flat regions. This drying may be done by heating or under vacuum.
- In some cases, it is desired to first rehydrate
  the droplets containing the analyte reagents to allow
  for more time for adsorption to the solid support. It
  is also possible to spot out the analyte reagents in a
  humid environment so that droplets do not dry until the
  arraying operation is complete.

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### III. Automated Apparatus for Forming Arrays

In another aspect, the invention includes an automated apparatus for forming an array of analyte-assay regions on a solid support, where each region in the array has a known amount of a selected, analyte-specific reagent.

The apparatus is shown in planar, and partially schematic view in Fig. 4. A dispenser device 72 in the apparatus has the basic construction described above with respect to Fig. 1, and includes a dispenser 74 having an open-capillary channel terminating at a tip, substantially as shown in Figs. 1 and 2A-2C.

The dispenser is mounted in the device for movement toward and away from a dispensing position at which the tip of the dispenser taps a support surface, to dispense a selected volume of reagent solution, as described above. This movement is effected by a solenoid 76 as described above. Solenoid 76 is under the control of a control unit 77 whose operation will be described below. The solenoid is also referred to herein as dispensing means for moving the device into tapping engagement with a support, when the device is positioned at a defined array position with respect to that support.

The dispenser device is carried on an arm 74 which is threadedly mounted on a worm screw 80 driven (rotated) in a desired direction by a stepper motor 82 also under the control of unit 77. At its left end in the figure screw 80 is carried in a sleeve 84 for rotation about the screw axis. At its other end, the screw is mounted to the drive shaft of the stepper motor, which in turn is carried on a sleeve 86. The dispenser device, worm screw, the two sleeves mounting the worm screw, and the stepper motor used in moving the device in the "x" (horizontal) direction in the

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described below.

figure form what is referred to here collectively as a displacement assembly 86.

The displacement assembly is constructed to produce precise, micro-range movement in the direction of the screw, i.e., along an x axis in the figure. In one mode, the assembly functions to move the dispenser in x-axis increments having a selected distance in the range 5-25 µm. In another mode, the dispenser unit may be moved in precise x-axis increments of several microns or more; for positioning the dispenser at associated positions on adjacent supports, as will be

The displacement assembly, in turn, is mounted for movement in the "y" (vertical) axis of the figure, for positioning the dispenser at a selected y axis position. The structure mounting the assembly includes a fixed rod 88 mounted rigidly between a pair of frame bars 90, 92, and a worm screw 94 mounted for rotation between a pair of frame bars 96, 98. The worm screw is driven (rotated) by a stepper motor 100 which converted

driven (rotated) by a stepper motor 100 which operates under the control of unit 77. The motor is mounted on bar 96, as shown.

The structure just described, including worm screw 94 and motor 100, is constructed to produce precise, 25 micro-range movement in the direction of the screw, i.e., along an y axis in the figure. As above, the structure functions in one mode to move the dispenser in y-axis increments having a selected distance in the range 5-250 µm, and in a second mode, to move the

dispenser in precise y-axis increments of several microns ( $\mu$ m) or more, for positioning the dispenser at associated positions on adjacent supports.

The displacement assembly and structure for moving this assembly in the y axis are referred to herein collectively as positioning means for positioning the

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dispensing device at a selected array position with respect to a support.

A holder 102 in the apparatus functions to hold a plurality of supports, such as supports 104 on which the microarrays of regent regions are to be formed by the apparatus. The holder provides a number of recessed slots, such as slot 106, which receive the supports, and position them at precise selected positions with respect to the frame bars on which the dispenser moving means is mounted.

As noted above, the control unit in the device functions to actuate the two stepper motors and dispenser solenoid in a sequence designed for automated operation of the apparatus in forming a selected microarray of reagent regions on each of a plurality of supports.

The control unit is constructed, according to conventional microprocessor control principles, to provide appropriate signals to each of the solenoid and each of the stepper motors, in a given timed sequence and for appropriate signalling time. The construction of the unit, and the settings that are selected by the user to achieve a desired array pattern, will be understood from the following description of a typical apparatus operation.

Initially, one or more supports are placed in one or more slots in the holder. The dispenser is then moved to a position directly above a well (not shown) containing a solution of the first reagent to be dispensed on the support(s). The dispenser solenoid is actuated now to lower the dispenser tip into this well, causing the capillary channel in the dispenser to fill. Motors 82, 100 are now actuated to position the dispenser at a selected array position at the first of the supports. Solenoid actuation of the dispenser is

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then effective to dispense a selected-volume droplet of that reagent at this location. As noted above, this operation is effective to dispense a selected volume preferably between 2 pl and 2 nl of the reagent solution.

The dispenser is now moved to the corresponding position at an adjacent support and a similar volume of the solution is dispensed at this position. The process is repeated until the reagent has been dispensed at this preselected corresponding position on each of the supports.

Where it is desired to dispense a single reagent at more than two array positions on a support, the dispenser may be moved to different array positions at each support, before moving the dispenser to a new support, or solution can be dispensed at individual positions on each support, at one selected position, then the cycle repeated for each new array position.

To dispense the next reagent, the dispenser is

positioned over a wash solution (not shown), and the dispenser tip is dipped in and out of this solution until the reagent solution has been substantially washed from the tip. Solution can be removed from the tip, after each dipping, by vacuum, compressed air spray, sponge, or the like.

The dispenser tip is now dipped in a second reagent well, and the filled tip is moved to a second selected array position in the first support. The process of dispensing reagent at each of the

30 corresponding second-array positions is then carried as above. This process is repeated until an entire microarray of reagent solutions on each of the supports has been formed.

### 35 IV. Microarray Substrate

This section describes embodiments of a substrate having a microarray of biological polymers carried on the substrate surface. Subsection A describes a multicell substrate, each cell of which contains a microarray, and preferably an identical microarray, of distinct biopolymers, such as distinct polynucleotides, formed on a porous surface. Subsection B describes a microarray of distinct polynucleotides bound on a glass slide coated with a polycationic polymer.

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#### A. Multi-Cell Substrate

Fig. 9 illustrates, in plan view, a substrate 110 constructed according to the invention. The substrate has an 8 × 12 rectangular array 112 of cells, such as 15 cells 114, 116, formed on the substrate surface. With reference to Fig. 10, each cell, such as cell 114, in turn supports a microarray 118 of distinct biopolymers, such as polypeptides or polynucleotides at known, addressable regions of the microarray. Two such 20 regions forming the microarray are indicated at 120, and correspond to regions, such as regions 42, forming the microarray of distinct biopolymers shown in Fig. 3.

The 96-cell array shown in Fig. 9 has typically array dimensions between about 12 and 244 mm in width and 8 and 400 mm in length, with the cells in the array having width and length dimension of 1/12 and 1/8 the array width and length dimensions, respectively, i.e., between about 1 and 20 in width and 1 and 50 mm in length.

The construction of substrate is shown crosssectionally in Fig. 11, which is an enlarged sectional view taken along view line 124 in Fig. 9. The substrate includes a water-impermeable backing 126, such as a glass slide or rigid polymer sheet. Formed on the surface of the backing is a water-permeable film

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128. The film is formed of a porous membrane material, such as nitrocellulose membrane, or a porous web material, such as a nylon, polypropylene, or PVDF porous polymer material. The thickness of the film is preferably between about 10 and 1000  $\mu$ m. The film may be applied to the backing by spraying or coating uncured material on the backing, or by applying a preformed membrane to the backing. The backing and film may be obtained as a preformed unit from commercial source, e.g., a plastic-backed nitrocellulose film available from Schleicher and Schuell Corporation.

With continued reference to Fig. 11, the filmcovered surface in the substrate is partitioned into a desired array of cells by water-impermeable grid lines, such as lines 130, 132, which have infiltrated the film down to the level of the backing, and extend above the surface of the film as shown, typically a distance of 100 to 2000 µm above the film surface.

The grid lines are formed on the substrate by laying down an uncured or otherwise flowable resin or elastomer solution in an array grid, allowing the material to infiltrate the porous film down to the backing, then curing or otherwise hardening the grid lines to form the cell-array substrate.

One preferred material for the grid is a flowable silicone available from Loctite Corporation. The barrier material can be extruded through a narrow syringe (e.g., 22 gauge) using air pressure or

30 mechanical pressure. The syringe is moved relative to the solid support to print the barrier elements as a grid pattern. The extruded bead of silicone wicks into the pores of the solid support and cures to form a shallow waterproof barrier separating the regions of

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In alternative embodiments, the barrier element can be a wax-based material or a thermoset material such as epoxy. The barrier material can also be a UV-curing polymer which is exposed to UV light after being printed onto the solid support. The barrier material may also be applied to the solid support using printing techniques such as silk-screen printing. The barrier material may also be a heat-seal stamping of the porous solid support which seals its pores and forms a waterimpervious barrier element. The barrier material may also be a shallow grid which is laminated or otherwise adhered to the solid support.

In addition to plastic-backed nitrocellulose, the solid support can be virtually any porous membrane with or without a non-porous backing. Such membranes are readily available from numerous vendors and are made from nylon, PVDF, polysulfone and the like. In an alternative embodiment, the barrier element may also be used to adhere the porous membrane to a non-porous backing in addition to functioning as a barrier to prevent cross contamination of the assay reagents.

In an alternative embodiment, the solid support can be of a non-porous material. The barrier can be printed either before or after the microarray of biomolecules is printed on the solid support.

As can be appreciated, the cells formed by the grid-lines and the underlying backing are water-impermeable, having side barriers projecting above the porous film in the cells. Thus, defined-volume samples can be placed in each well without risk of cross-contamination with sample material in adjacent cells. In Fig. 11, defined volumes samples, such as sample 134, are shown in the cells.

As noted above, each well contains a microarray of distinct biopolymers. In one general embodiment, the

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microarrays in the well are identical arrays of distinct biopolymers, e.g., different sequence polynucleotides. Such arrays can be formed in accordance with the methods described in Section II, by depositing a first selected polynucleotide at the same selected microarray position in each of the cells, then depositing a second polynucleotide at a different microarray position in each well, and so on until a complete, identical microarray is formed in each cell.

In a preferred embodiment, each microarray contains about 10° distinct polynuclectide or polypeptide biopolymers per surface area of less than about 1 cm². Also in a preferred embodiment, the biopolymers in each microarray region are present in a defined amount between about 0.1 femtomoles and 100 nanomoles. The ability to form high-density arrays of biopolymers, where each region is formed of a well-defined amount of deposited material, can be achieved in accordance with the microarray-forming method described in Section II.

Also in a preferred embodiments, the biopolymers are polynucleotides having lengths of at least about 50 bp, i.e., substantially longer than oligonucleotides which can be formed in high-density arrays by schemes involving parallel, step-wise polymer synthesis on the array surface.

In the case of a polynucleotide array, in an assay procedure, a small volume of the labeled DNA probe mixture in a standard hybridization solution is loaded onto each cell. The solution will spread to cover the entire microarray and stop at the barrier elements. The solid support is then incubated in a humid chamber at the appropriate temperature as required by the assay.

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Each assay may be conducted in an "open-face" format where no further sealing step is required, since the hybridization solution will be kept properly hydrated by the water vapor in the humid chamber. the conclusion of the incubation step, the entire solid support containing the numerous microarrays is rinsed quickly enough to dilute the assay reagents so that no significant cross contamination occurs. The entire solid support is then reacted with detection reagents if needed and analyzed using standard colorimetric, 10 radioactive or fluorescent detection means. All processing and detection steps are performed simultaneously to all of the microarrays on the solid support ensuring uniform assay conditions for all of the microarrays on the solid support. 15

#### B. Glass-Slide Polynucleotide Array

Fig. 5 shows a substrate 136 formed according to another aspect of the invention, and intended for use in detecting binding of labeled polynucleotides to one or more of a plurality distinct polynucleotides. The substrate includes a glass substrate 138 having formed on its surface, a coating of a polycationic polymer, preferably a cationic polypeptide, such as polylysine or polyarginine. Formed on the polycationic coating is a microarray 140 of distinct polynucleotides, each localized at known selected array regions, such as regions 142.

The slide is coated by placing a uniform-thickness

film of a polycationic polymer, e.g., poly-1-lysine, on
the surface of a slide and drying the film to form a
dried coating. The amount of polycationic polymer
added is sufficient to form at least a monolayer of
polymers on the glass surface. The polymer film is
bound to surface via electrostatic binding between

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negative silyl-OH groups on the surface and charged amine groups in the polymers. Poly-1-lysine coated glass slides may be obtained commercially, e.g., from Sigma Chemical Co. (St. Louis, MO).

To form the microarray, defined volumes of distinct polynucleotides are deposited on the polymer-coated slide, as described in Section II. According to an important feature of the substrate, the deposited polynucleotides remain bound to the coated slide surface non-covalently when an aqueous DNA sample is applied to the substrate under conditions which allow hybridization of reporter-labeled polynucleotides in the sample to complementary-sequence (single-stranded) polynucleotides in the substrate array. The method is illustrated in Examples 1 and 2.

To illustrate this feature, a substrate of the type just described, but having an array of same-sequence polynucleotides, was mixed with fluorescent-labeled complementary DNA under hybridization conditions. After washing to remove non-hybridized material, the substrate was examined by low-power fluorescence microscopy. The array can be visualized by the relatively uniform labeling pattern of the array regions.

25 In a preferred embodiment, each microarray contains at least 10<sup>3</sup> distinct polynucleotide or polypeptide biopolymers per surface area of less than about 1 cm<sup>2</sup>. In the embodiment shown in Fig. 5, the microarray contains 400 regions in an area of about 16 mm<sup>2</sup>, or 2.5 × 10<sup>3</sup> regions/cm<sup>2</sup>. Also in a preferred embodiment, the polynucleotides in the each microarray region are present in a defined amount between about 0.1 femtomoles and 100 nanomoles in the case of polynucleotides. As above, the ability to form high-

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density arrays of this type, where each region is formed of a well-defined amount of deposited material, can be achieved in accordance with the microarrayforming method described in Section II.

Also in a preferred embodiments, the polynucleotides have lengths of at least about 50 bp, i.e., substantially longer than oligonucleotides which can be formed in high-density arrays by various in situ synthesis schemes.

#### V. Utility

Microarrays of immobilized nucleic acid sequences prepared in accordance with the invention can be used for large scale hybridization assays in numerous

15 genetic applications, including genetic and physical mapping of genomes, monitoring of gene expression, DNA sequencing, genetic diagnosis, genotyping of organisms, and distribution of DNA reagents to researchers.

For gene mapping, a gene or a cloned DNA fragment 20 is hybridized to an ordered array of DNA fragments, and the identity of the DNA elements applied to the array is unambiguously established by the pixel or pattern of pixels of the array that are detected. One application of such arrays for creating a genetic map is described 25 by Nelson, et al. (1993). In constructing physical maps of the genome, arrays of immobilized cloned DNA fragments are hybridized with other cloned DNA fragments to establish whether the cloned fragments in the probe mixture overlap and are therefore contiguous 30 to the immobilized clones on the array. For example, Lehrach, et al., describe such a process.

The arrays of immobilized DNA fragments may also be used for genetic diagnostics. To illustrate, an array containing multiple forms of a mutated gene or genes can be probed with a labeled mixture of a

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patient's DNA which will preferentially interact with only one of the immobilized versions of the gene.

The detection of this interaction can lead to a medical diagnosis. Arrays of immobilized DNA fragments can also be used in DNA probe diagnostics. For example, the identity of a pathogenic microorganism can be established unambiguously by hybridizing a sample of the unknown pathogen's DNA to an array containing many types of known pathogenic DNA. A similar technique can also be used for unambiguous genotyping of any organism. Other molecules of genetic interest, such as CDNA's and RNA's can be immobilized on the array or alternately used as the labeled probe mixture that is applied to the array.

In one application, an array of cDNA clones representing genes is hybridized with total cDNA from an organism to monitor gene expression for research or diagnostic purposes. Labeling total cDNA from a normal cell with one color fluorophore and total cDNA from a diseased cell with another color fluorophore and simultaneously hybridizing the two cDNA samples to the same array of cDNA clones allows for differential gene expression to be measured as the ratio of the two fluorophore intensities. This two-color experiment can be used to monitor gene expression in different tissue types, disease states, response to drugs, or response to environmental factors. & An example of this approach is illustrated in Examples 2, described with respect to Fig. 8.

By way of example and without implying a limitation of scope, such a procedure could be used to simultaneously screen many patients against all known mutations in a disease gene. This invention could be used in the form of, for example, 96 identical 0.9 cm × 2.2 cm microarrays fabricated on a single 12 cm × 18 cm

WO 95/35505

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sheet of plastic-backed nitrocellulose where each microarray could contain, for example, 100 DNA fragments representing all known mutations of a given gene. The region of interest from each of the DNA samples from 96 patients could be amplified, labeled, and hybridized to the 96 individual arrays with each assay performed in 100 microliters of hybridization solution. The approximately 1 thick silicone rubber barrier elements between individual arrays prevent cross contamination of the patient samples by sealing 10 the pores of the nitrocellulose and by acting as a physical barrier between each microarray. The solid support containing all 96 microarrays assayed with the 96 patient samples is incubated, rinsed, detected and 15 analyzed as a single sheet of material using standard radioactive, fluorescent, or colorimetric detection means (Maniatas, et al., 1989). Previously, such a procedure would involve the handling, processing and tracking of 96 separate membranes in 96 separate sealed chambers. By processing all 96 arrays as a single 20 sheet of material, significant time and cost savings are possible.

The assay format can be reversed where the patient or organism's DNA is immobilized as the array elements and each array is hybridized with a different mutated allele or genetic marker. The gridded solid support can also be used for parallel non-DNA ELISA assays. Furthermore, the invention allows for the use of all standard detection methods without the need to remove the shallow barrier elements to carry out the detection step.

In addition to the genetic applications listed above, arrays of whole cells, peptides, enzymes, antibodies, antigens, receptors, ligands,

35 phospholipids, polymers, drug cogener preparations or

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chemical substances can be fabricated by the means described in this invention for large scale screening assays in medical diagnostics, drug discovery, molecular biology, immunology and toxicology.

The multi-cell substrate aspect of the invention allows for the rapid and convenient screening of many DNA probes against many ordered arrays of DNA fragments. This eliminates the need to handle and detect many individual arrays for performing mass screenings for genetic research and diagnostic applications. Numerous microarrays can be fabricated on the same solid support and each microarray reacted with a different DNA probe while the solid support is processed as a single sheet of material.

The following examples illustrate, but in no way are intended to limit, the present invention.

#### Example 1

Genomic-Complexity Hybridization to Micro
DNA Arrays Representing the Yeast
Saccharomyces cerevisiae Genome with
Two-Color Fluorescent Detection

The array elements were randomly amplified PCR (Bohlander, et al., 1992) products using physically mapped lambda clones of S. cerevisiae genomic DNA templates (Riles, et al., 1993). The PCR was performed directly on the lambda phage lysates resulting in an amplification of both the 35 kb lambda vector and the

30 5-15 kb yeast insert sequences in the form of a uniform distribution of PCR product between 250-1500 base pairs in length. The PCR product was purified using Sephadex G50 gel filtration (Pharmacia, Piscataway, NJ) and concentrated by evaporation to dryness at room

35 temperature overnight. Each of the 864 amplified

WO 95/35505 PCT/US95/07659

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lambda clones was rehydrated in 15  $\mu l$  of 3  $\times$  SSC in preparation for spotting onto the glass.

The micro arrays were fabricated on microscope slides which were coated with a layer of poly-1-lysine (Sigma). The automated apparatus described in Section IV loaded 1  $\mu$ l of the concentrated lambda clone PCR product in 3 x SSC directly from 96 well storage plates into the open capillary printing element and deposited -5 nl of sample per slide at 380 micron spacing between spots, on each of 40 slides. The process was repeated 10 for all 864 samples and 8 control spots. After the spotting operation was complete, the slides were rehydrated in a humid chamber for 2 hours, baked in a dry 80° vacuum oven for 2 hours, rinsed to remove unabsorbed DNA and then treated with succinic anhydride 15 to reduce non-specific adsorption of the labeled hybridization probe to the poly-1-lysine coated glass surface. Immediately prior to use, the immobilized DNA on the array was denatured in distilled water at 90° 20 for 2 minutes.

For the pooled chromosome experiment, the 16 chromosomes of Saccharomyces cerevisiae were separated in a CHEF agarose gel apparatus (Biorad, Richmond, CA). The six largest chromosomes were isolated in one gel slice and the smallest 10 chromosomes in a second gel 25 slice. The DNA was recovered using a gel extraction kit (Qiagen, Chatsworth, CA). The two chromosome pools were randomly amplified in a manner similar to that used for the target lambda clones. Following amplification, 5 micrograms of each of the amplified 30 chromosome pools were separately random-primer labeled using Klenow polymerase (Amersham, Arlington Heights, IL) with a lissamine conjugated nucleotide analog (Dupont NEN, Boston, MA) for the pool containing the six largest chromosomes, and with a fluorescein 35

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conjugated nucleotide analog (BMB) for the pool containing smallest ten chromosomes. The two pools were mixed and concentrated using an ultrafiltration device (Amicon, Danvers, MA).

Five micrograms of the hybridization probe consisting of both chromosome pools in 7.5  $\mu$ l of TE was denatured in a boiling water bath and then snap cooled on ice. 2.5  $\mu$ l of concentrated hybridization solution (5 × SSC and 0.1% SDS) was added and all 10  $\mu$ l transferred to the array surface, covered with a cover slip, placed in a custom-built single-slide humidity chamber and incubated at 60° for 12 hours. The slides were then rinsed at room temperature in 0.1 × SSC and

0.14SDS for 5 minutes, cover slipped and scanned.

A custom built laser fluorescent scanner was used to detect the two-color hybridization signals from the 1.8 x 1.8 cm array at 20 micron resolution. The scanned image was gridded and analyzed using custom image analysis software. After correcting for optical crosstalk between the fluorophores due to their overlapping emission spectra, the red and green hybridization values for each clone on the array were correlated to the known physical map position of the clone resulting in a computer-generated color karyotype of the yeast genome.

Figure 6 shows the hybridization pattern of the two chromosome pools. A red signal indicates that the lambda clone on the array surface contains a cloned genomic DNA segment from one of the largest six yeast chromosomes. A green signal indicates that the lambda clone insert comes from one of the smallest ten yeast chromosomes. Orange signals indicate repetitive sequences which cross hybridized to both chromosome pools. Control spots on the array confirm that the hybridization is specific and reproducible.

The physical map locations of the genomic DNA fragments contained in each of the clones used as array elements have been previously determined by Olson and co-workers (Riles, et al.) allowing for the automatic generation of the color karyotype shown in Figure 7. The color of a chromosomal section on the karvotype Corresponds to the color of the array element containing the clone from that section. The black regions of the karyotype represent false negative dark 10 spots on the array (10%) or regions of the genome not covered by the Olson clone library (90%). Note that the largest six chromosomes are mainly red while the smallest ten chromosomes are mainly green matching the original CHEF gel isolation of the hybridization probe. 15 Areas of the red chromosomes containing green spots and vice-versa are probably due to spurious sample tracking

The yeast genome arrays have also been probed with individual clones or pools of clones that are fluorescently labeled for physical mapping purposes. The hybridization signals of these clones to the array were translated into a position on the physical map of yeast.

errors in the formation of the original library and in

the amplification and spotting procedures.

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#### Example 2

# Total cDNA Hybridized to Micro Arrays of cDNA Clones with Two-Color Fluorescent Detection

24 clones containing cDNA inserts from the plant Arabidopsis were amplified using PCR. Salt was added to the purified PCR products to a final concentration of 3 x SSC. The cDNA clones were spotted on poly-lysine coated microscope slides in a manner similar to Example 1. Among the cDNA clones was a clone

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representing a transcription factor HAT 4, which had previously been used to create a transgenic line of the plant Arabidopsis, in which this gene is present at ten times the level found in wild-type Arabidopsis (Schena, et al., 1992).

Total poly-A mRNA from wild type Arabidopsis was isolated using standard methods (Maniatis, et al., 1989) and reverse transcribed into total cDNA, using fluorescein nucleotide analog to label the cDNA product (green fluorescence). A similar procedure was performed with the transgenic line of Arabidopsis where the transcription factor HAT4 was inserted into the genome using standard gene transfer protocols. cDNA copies of mRNA from the transgenic plant are labeled with a lissamine nucleotide analog (red fluorescence). Two micrograms of the cDNA products from each type of plant were pooled together and hybridized to the cDNA clone array in a 10 microliter hybridization reaction

detection of hybridization was also performed in a manner similar to Example 1. Fig. 8 show the resulting hybridization pattern of the array.

Rinsing and

in a manner similar to Example 1.

Genes equally expressed in wild type and the transgenic Arabidopsis appeared yellow due to equal contributions of the green and red fluorescence to the final signal. The dots are different intensities of yellow indicating various levels of gene expression. The cDNA clone representing the transcription factor HAT4, expressed in the transgenic line of Arabidopsis but not detectably expressed in wild type Arabidopsis, appears as a red dot (with the arrow pointing to it), indicating the preferential expression of the transcription factor in the red-labeled transgenic Arabidopsis and the relative lack of expression of the

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transcription factor in the green-labeled wild type Arabidopsis.

An advantage of the microarray hybridization format for gene expression studies is the high partial concentration of each cDNA species achievable in the 10 microliter hybridization reaction. This high partial concentration allows for detection of rare transcripts without the need for PCR amplification of the hybridization probe which may bias the true genetic representation of each discrete cDNA species.

Gene expression studies such as these can be used for genomics research to discover which genes are expressed in which cell types, disease states, development states or environmental conditions. Gene expression studies can also be used for diagnosis of disease by empirically correlating gene expression patterns to disease states.

#### Example 3

## Multiplexed Colorimetric Hybridization on a Gridded Solid Support

A sheet of plastic-backed nitrocellulose was gridded with barrier elements made from silicone rubber according to the description in Section IV-A. The

sheet was soaked in 10 x SSC and allowed to dry. As shown in Fig. 12, 192 M13 clones each with a different yeast inserts were arrayed 400 microns apart in four quadrants of the solid support using the automated device described in Section III. The bottom left quadrant served as a negative control for hybridization while each of the other three quadrants was hybridized simultaneously with a different oligonucleotide using the open-face hybridization technology described in Section IV-A. The first two and last four elements of

each array are positive controls for the colorimetric detection step.

The oligonucleotides were labeled with fluorescein which was detected using an anti-fluorescein antibody conjugated to alkaline phosphatase that precipitated an NBT/BCIP dye on the solid support (Amersham). Perfect matches between the labeled oligos and the M13 clones resulted in dark spots visible to the naked eye and detected using an optical scanner (HP ScanJet II) attached to a personal computer. The hybridization 10 patterns are different in every quadrant indicating that each oligo found several unique M13 clones from among the 192 with a perfect sequence match. Note that the open capillary printing tip leaves detectable dimples on the nitrocellulose which can be used to automatically align and analyze the images.

Although the invention has been described with respect to specific embodiments and methods, it will be 20 clear that various changes and modification may be made without departing from the invention.

#### IT IS CLAIMED:

- A method of forming a microarray of analyteassay regions on a solid support, where each region in the array has a known amount of a selected, analytespecific reagent, said method comorising.
  - (a) loading a solution of a selected analyte-specific reagent in a reagent-dispensing device having an elongate capillary channel (i) formed by spaced-apart, coextensive elongate members, (ii) adapted to hold a quantity of the reagent solution and (iii) having a tip region at which aqueous solution in the channel forms a meniscus,
- (b) tapping the tip of the dispensing device 15 against a solid support at a defined position on the surface, with an impulse effective to break the meniscus in the capillary channel and deposit a selected volume of solution on the surface, and
- (c) repeating steps (a) and (b) until said array 20 is formed.
- The method of claim 1, wherein said tapping is carried out with an impulse effective to deposit a selected volume in the volume range between 0.01 to 100
   n1.
  - The method of claim 1, wherein said channel is formed by a pair of spaced-apart tapered elements.
- 4. The method of claim 1, for forming a plurality of such arrays, wherein step (b) is applied to a selected position on each of a plurality of solid supports at each repeat cycle proceeding step (c).

- 5. The method of claim 1, which further includes, after performing steps (a) and (b) at least one time, reloading the reagent-dispensing device with a new reagent solution by the steps of (i) dipping the capillary channel of the device in a wash solution, (ii) removing wash solution drawn into the capillary channel, and (iii) dipping the capillary channel into the new reagent solution.
- 6. Automated apparatus for forming a microarray of analyte-assay regions on a plurality of solid supports, where each region in the array has a known amount of a selected, analyte-specific reagent, said apparatus comprising
- (a) a holder for holding, at known positions, a plurality of planar supports,
  - (b) a reagent dispensing device having an open capillary channel (i) formed by spaced-apart,coextensive elongate members (ii) adapted to hold a
- 20 quantity of the reagent solution and (iii) having a tip region at which aqueous solution in the channel forms a meniscus.
  - (c) positioning means for positioning the dispensing device at a selected array position with respect to a support in said holder,
    - (d) dispensing means for moving the device into tapping engagement against a support with a selected impulse, when the device is positioned at a defined array position with respect to that support, with an
- 30 impulse effective to break the meniscus of liquid in the capillary channel and deposit a selected volume of solution on the surface, and
  - (e) control means for controlling said positioning and dispensing means.

WO:95/35505

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- 7. The apparatus of claim 6, wherein said dispensing means is effective to move said dispensing device against a support with an impulse effective to deposit a selected volume in the volume range between 0.01 to 100 nl.
- The apparatus of claim 6, wherein said channel is formed by a pair of spaced-apart tapered elements.
- 9. The apparatus of claim 6, wherein the control means operates to (i) place the dispensing device at a loading station, (ii) move the capillary channel in the device into a selected reagent at the loading station, to load the dispensing device with the reagent, and (iii) dispense the reagent at a defined array position on each of the supports on said holder.
  - 10. The apparatus of claim 6, wherein the control device further operates, at the end of a dispensing cycle, to wash the dispensing device by (i) placing the dispensing device at a washing station, (ii) moving the capillary channel in the device into a wash fluid, to load the dispensing device with the fluid, and (iii) remove the wash fluid prior to loading the dispensing device with a fresh selected reagent.
  - 11. The apparatus of claim 6, wherein said device is one of a plurality of such devices which are carried on the arm for dispensing different analyte assay reagents at selected spaced array positions.
    - 12. A substrate with a surface having a microarray of at least 10<sup>3</sup> distinct polynucleotide or polypeptide biopolymers per 1 cm<sup>2</sup> surface area, each

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distinct biopolymer sample (i) being disposed at a separate, defined position in said array, (ii) having a length of at least 50 subunits, and (iii) being present in a defined amount between about 0.1 femtomole and 100 nanomoles.

- 13. The substrate of claim 12, wherein said surface is glass slide coated with polylysine, and said biopolymers are polynucleotides.
- 14. The substrate of claim 12, wherein said substrate has a water-impermeable backing, a water-permeable film formed on the backing, and a grid formed on the film, where said grid (i) is composed of intersecting water-impervious grid elements extending from said backing to positions raised above the surface of said film, and (ii) partitions the film into a plurality of water-impervious cells, where each cell contains such a biopolymer array.
- 15. A substrate with a surface array of sample-receiving cells, comprising
  - a water-impermeable backing,
- a water-permeable film formed on the backing, and 25 a grid formed on the film, said grid being composed of intersecting water-impervious grid elements extending from said backing to positions raised above the surface of said film.
- 30 16. The substrate of claim 15, wherein the cells of the array each contain an array of biopolymers.
- A substrate for use in detecting binding of labeled biopolymers to one or more of a plurality distinct polynucleotides, comprising

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- a non-porous, glass substrate,
- a coating of a cationic polymer on said substrate, and
- an array of distinct polynucleotides to said coating, where each biopolymer is disposed at a separate, defined position in a surface array of biopolymers.
- 18. A method of detecting differential expression 10 of each of a plurality of genes in a first cell type with respect to expression of the same genes in a second cell types, said method comprising

producing fluorescence-labeled cDNA's from mRNA's isolated from the two cells types, where the cDNA's from the first and second cells are labeled with first and second different fluorescent reporters,

adding a mixture of the labeled cDNA's from the two cell types to an array of polynucleotides representing a plurality of known genes derived from the two cell types, under conditions that result in hybridization of the cDNA's to complementary-sequence polynucleotides in the array; and

examining the array by fluorescence under fluorescence excitation conditions in which (i)

25 polynucleotides in the array that are hybridized predominantly to cDNA's derived from one of the first and second cell types give a distinct first or second fluorescence emission color, respectively, and (ii) polynucleotides in the array that are hybridized to

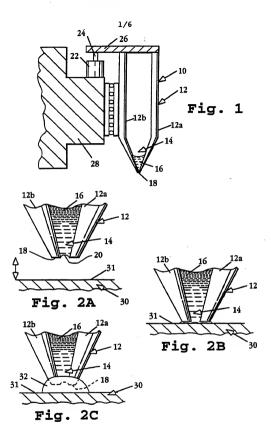
30 substantially equal numbers of cDNA's derived from the first and second cell types give a distinct combined fluorescence emission color, respectively,

wherein the relative expression of known genes in the two cell types can be determined by the observed fluorescence emission color of each spot. 19. The method of claim 18, wherein the array of polynucleotides is formed on a substrate with a surface having an array of at least 10<sup>2</sup> distinct polynucleotide or polypeptide biopolymers in a surface area of less than about 1 cm<sup>2</sup>, each distinct biopolymer (i) being disposed at a separate, defined position in said array, (ii) having a length of at least 50 subunits, and (iii) being present in a defined amount between about .1 femtomole and 100 nmoles.

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20. The method of claim 19, wherein said surface is a glass slide coated with polylysine, and said biopolymers are polynucleotides non-covalently bound to said polylysine. WO 95/35505



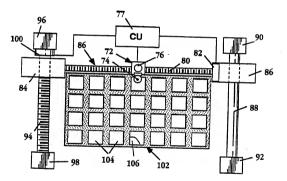


Fig. 4



Fig. 5

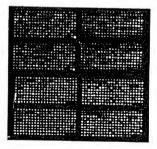


Fig. 6

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Fig. 7

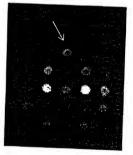
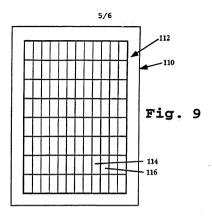


Fig. 8

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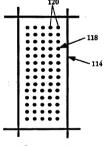
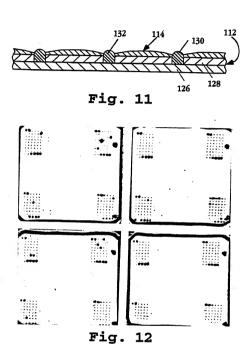


Fig. 10



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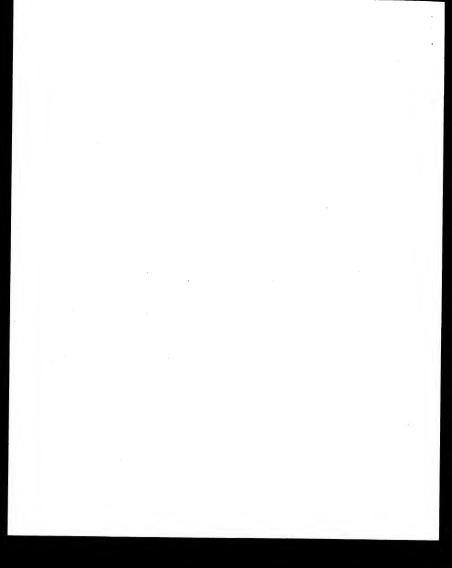
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| iske Grant (London)                                |                   | Detical accessor accessor accessor accessor in Laborator  | 461 |
| Assistant Classified Sales                         |                   | Retinal-specific guanylate cyclase gene mutations in Leber's<br>congenital amaurosis  | 461 |
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| Production & Information<br>Systems Director       |                   | J-L Dufier, S Pittler, A Munnich & J Kaplan   |     |
| Nick Kemp  |                   | Complex into a state of a second control to the first   | 465 |
| Circulation Manager                                |                   | Complex interactions of new quantitative trait loci, Sluc1, Sluc2, Sluc3, and Sluc4, that influence the susceptibility to lung  | 405 |
| Moira Musto (New York)                             |                   | cancer in the mouse   |     |
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| na Dzurenda  |                   | Gene interaction and single gene effects in colon tumour<br>susceptibility in mice  | 400 |
|  |                   | T van Wezel, A P M Stassen, C J A Moen, A A M Hart, M A van der Valk &  |     |
|  |                   | P Demant 116-11   |     |
| <b>*</b>   |                   |   |     |
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| Andy Sutherialio                                   |                   | Homozygosity mapping of Hallervorden-Spatz syndrome to  | 479 |
| Editor-in-Chief,                                   |                   | chromosome 20p12.3-p13 T D Taylor, M Litt, P Kramer, M Pandolfo, L Angelini, N Nardocci, S Davis,   |     |
| Nature publications Philip Campbell                |                   | M Pineda, H Hattori, P J Flett, M R Cilio, E Bertini & S J Hayflick   |     |
|  |                   |   |     |
| Art Director<br>Jane Walker                        | •                 | Identification of BTG2, an antiproliferative p53-dependent  | 482 |
| etine rraine.                                      |                   | component of the DNA damage cellular response pathway   |     |
|  | _                 | J-P Rouault, N Falette, F Guéhenneux, C Guillot, R Rimokh, Q Wang,<br>C Berthet, C Movret-Lalle, P Savatier, B Pain, P Shaw, R Berger,  |     |
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### Use of a cDNA microarray to analyse gene expression patterns in human cancer

Joseph DeRisi<sup>1+</sup>, Lolita Penland<sup>2</sup> & Patrick O. Brown<sup>2</sup> (Group 1); Michael L. Bittner<sup>1+</sup>, Paul S. Meltzer<sup>3</sup>, Michael Ray<sup>3</sup>, Yidong Chen<sup>3</sup>, Yan A. Su<sup>3</sup> & Jeffrey M. Trent<sup>3</sup> (Group 2)

The development and progression of cancer 1-3 and the experimental reversal of tumorigenicity<sup>4,5</sup> are accompanied by complex changes in patterns of gene expression. Microarrays of cDNA provide a powerful tool for studying these complex phenomena<sup>6-8</sup>. The tumorigenic properties of a human melanoma cell line. UACC-903, can be suppressed by introduction of a normal human chromosome 6. resulting in a reduction of growth rate, restoration of contact inhibition, and suppression of both soft agar clonogenicity and tumorigenicity in nude mice4.5.9. We used a high density microarray of 1.161 DNA elements to search for differences in gene expression associated with tumour suppression in this system. Fluorescent probes for hybridization were derived from two sources of cellular mRNA [UACC-903 and UACC-903(+6)] which were labelled with different fluors to provide a direct and internally controlled comparison of the mRNA levels corresponding to each arrayed gene. The fluorescence signals representing hybridization to each arrayed gene were analysed to determine the relative abundance in the two samples of mRNAs corresponding to each gene. Previously unrecognized alterations in the expression of specific genes provide leads for further investigation of the genetic basis of the tumorigenic phenotype of these cells.

DNA microarrays, containing 1,161 total elements. including 870 different cDNAs and controls9-11 (see Methods), were printed robotically onto a glass microscope slide in four quadrants covering an area of about 1 cm2 (Fig. 1). We prepared fluorescent cDNA probes using total poly (A)\* mRNA from UACC-903 cells and UACC-903(+6) cells by labelling with a green and red fluor, respectively. A mixture of the two flourescently labelled probes was hybridized to the DNA microarray. This comparative hybridization method, coupled with the doping of synthetic standards and an estimation of statistically significant deviation for local background variance allowed a direct and quantitative comparison of the relative abundance of individual DNA sequences in this complex sample6-8. We added a set of synthetic poly (A)\*-tailed 'mRNAs' to the purified mRNA from each cell line as internal standards to assist in quantitation and estimation of experimental variation introduced during labelling and reading. Targets complementary to these standards were included, in duplicate, on the microarray, Based on these standards, mRNA species comprising 1:10,000 of the mass of the poly (A)\* RNA could readily be detected.

In a representative two-colour fluorescent scan of all LHO arrays following (Fig. 2a), the green spoke colors

spond to genes preferentially expressed in the tumorigenic UACC-903 cell line, and the reddish spots correspond to genes preferentially expressed in the non-tumorigenic UACC-903(+6) cell line. Genes expressed at approximately equal levels in the two cell lines appear yellow or brown. A portion of the array at higher magnification highlights the diverse pattern of differential expression observed (Fig. 2b). In Fig. 2c, rectangles corresponding to specific array elements are coloured to reproduce the hue and intensity of the fluorescent signal at each element. The hybridization signals from a duplicated set of genes are shown juxtaposed, to illustrate the reproducibility of the hybridization signals for each gene.

To address the possibility that an apparent difference in expression might result from experimental variables unrelated to the difference in chromosomal composition between the two cell lines, we examined the variance in expression for 90 'housekeeping' genes. We selected these genes based on the assumption that they would not be differentially expressed between the two cell lines. The averaged red/green ratio for this subset of genes was 1.13. The averaged red/green ratio for the set of five internal standards was 0.97 (n = 10). The variability in the expression level of the housekeeping genes probably overestimates the experimental variability in measuring differential expression. As a conservative standard, an absolute fluorescent signal (red or green) with an intensity greater than that observed at the control array elements containing total human genomic DNA was considered to represent specific hybridization. Genespecific hybridization was therefore only considered significantly different between samples if the following two criteria were met: i) the signal intensity (green or red) exceeded this threshold; and ii) the logarithm of the red/green fluorescence signal ratio differed by ≥3 S.D. from the mean logarithm of this ratio for the housekeeping' gene panel (that is, ratios <0.52 or >2.4).

by these criteria, mRNA levels for 15/870 (1.7%) genes were significantly diminished, while the mRNA levels for 63/870 (7.7%) genes were significantly increased in association with suppression of tumorigenicity by introduction of chromosome 6. To test the reliability of microarray hybridization results in identifying differentially expressed genes, we analysed 16 genes by norther analysis. In each case, the results of northern analysis corroborated the differential gene expression identified by microarray hybridization (Fig. 3).

Significant differences in expression between these two cell lines identified several genes as candidates for determining features of the tumorigenic phenotype of the melanoma cells. For example, among the genes detected with significantly higher expression (>10-fold) in the tumorigenic cells was the human brown locus protein (TRP1/melanoma antigen gp75). This is the most abundant glycoprotein in melanocytic cells and a critical melanosome membrane protein 12.13. Additionally, its expression is reduced when melanoma cell lines are induced to differentiate by treatment with HMBA12,13 Also expressed at a significantly higher level was a spliced variant of the mRNA encoding myelin PLP/DM20. This is widely expressed in neural crest derived cells in early development and has been suggested to play a role in cell-cell signaling during development14

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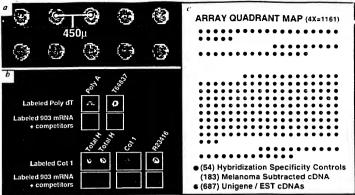


Fig. 1 Properties of cDNA microarrays, a. A fluorescent scan of DNA printed onto a poly-typer coates state. The DNA is stained with a DNA-specific fluorescent dive. VOVO. The center-to-center spacing of adjacent spots in \$50, allowing the potential for up to 10,000 solotos/2.84 x 16 and microscope state. B. Efficient blocking of hyprodization to DNA repeats, hyprodization for productions and the production of the production of productions of the production o

els were elevated by the addition of a normal chromosome 6 (17 genes) are known to be activated by IFN-Y, a cardinal proinflammatory cytokine that, among other activities, induces expression of the gene products of the MHC class II locus. For example, the mRNA encoding monocyte chemotactic protein 1 (MCAF/MCP1), a cytokine that induces monocyte chemotaxis and activation 15.16, was more than 10-fold less abundant in the tumorigenic cell line. In the skin, MPC1 is critical in the regulation of cutaneous monocyte trafficking 10-17, and elevated expression plays a role in suppression of tumour growth and metastasis 19-21. The mechanism by which these interferon-y regulated genes are induced in UACC-903 cells by transfer of a normal chromosome 6 remains to be determined. It is worth noting, however, that the interferon-y receptor gene is localized to the distal long arm of human chromosome 6.

Finally, several genes that showed >10-fold higher expression in the suppressed UACC-903(+6) cells have previously been recognized in other models of tumour suppression. Most notably, there was elevated expression of the mRNA encoding WAFI (p21), a key mediator of tumour suppression by p53 (ref. 18). The p21 protein had previously been identified as a melanoma differentiation-associated antigen (termed mda-6)<sup>19-20</sup>. In melanoma cell lines suppressed for metastasis by the introduction of chromosome 6, expression of WAFI (p21) mRNA and protein correlates inversely with metastatic potential<sup>20</sup>.

These results provide a wide view of the diverse systems that are altered in this model system of tumorigenicity, and focus attention on specific gene products and pathways that may be of particular importance in this tumour type.

Our ability to classify human cancers in a way that reflects the underlying molecular pathology or that anticipates their potential for progression or response to treatment, remains primitive. Using cDNA microarrays to define alterations in gene expression associated with a specific cancer may be an efficient way to uncovercluse to the specific molecular detangements that contribute to its pathogenesis and thus identify potential targets for therapeutic intervention. Moreover, recognition of pathognomonic alterations in gene expression might provide a basis for improved diagnosis and molecular classification of cancers and thus allow selection of the most appropriate therapeutic strategies.

Public databases of human expressed gene sequences contain partial sequences of at least 40,000 different human genes!, and efforts to develop a human transcript map have developed rapidly?! Based on the high yield of information obtained using an array of <1,000 different genes, a more comprehensive survey of gene expression patterns, using a more complete array of human genes, will likely provide a rich source of new and useful insights into human biology and a deeper understanding of the gene pathways involved in the pathogenesis of cancer and other diseases.

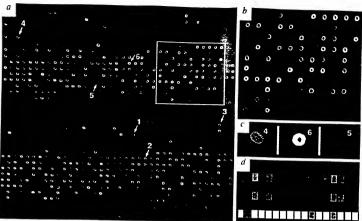


Fig. 2 DNA increasing analysis of changes in gene expression between the tumorgenic cell line. UACC-903, and its non-tumorgenic derivative. UACC-903 and its non-tumorgenic derivative. UACC-903 and (15) absolute of the common o

#### Methods

Generation of microarrays, hybridization, scanning. The preparation of coated microscope slides and subsequent robotic printing of DNA was carried out in a manner similar to that described. Briefly, pre-cleaned glass slides were treated with poly-1-lysine solution (Sigma) to form an adhesive surface for priming, PCR products, purified by ethanol purification, were resuspended in 3x SSC. A custom built arraying robot picked up and deposited small volumes (+5 nanoliters) of DNA onto the slides. After printing, the slides were washed in a 0.2% SDS solution. The remaining bound DNA was denatured by submerging the slides in 95 °C distilled water for 2 min followed by a brief wash with 95% ethanol, DNA was UV crosslinked to the slides (Stratagene Stratalinker, 60 ml). To prevent non-specific probe binding, the slides were blocked by rinsing in a solution of 70 mM succinic anhydride dissolved in 0.1 M boric acid pH 8.0, containing 35% 1-methyl-2-pyrrolidinone (Aldrich). Additional protocols and parts list pertaining to microarray labrication can be obtained from http://emgm.stanford.edu/

Purified, Idelical CDAA was resospended in 11 pt on 3.58 SSC containing slip of poly (doA) (DNA, 2.5 pg E. rofi (BNA, 4 pg of human Cut LDNA (Cubon BBL), and 0.3 pt of 10% SDS. Prior to hybridaziono, the solution was builed for 2 mm then allowed to coul to from temperature. LDNa/buildation was certified out of 62 °C for -44 h in a water bath. Prior to scinning, slides were waden by SSC, 0.2% SDS for 5 mm and 12% SSC for 1 mm, had been a solution of the solution of the solution of the boal laser microscope built by S. Smith with software withou by N. Ziv. A separate scan, using the appropriate excitation line, was done for each of the two fluorophores used. Data was collected at a maximum resolution of 9 microns/pixel with 12 bits of depth.

Probe preparation and labelling, RNA was extracted from cells toming the Trazon reagent HTI Inc.), following the manufacturer's directions, cDNA profices were synthesized from singly oligiod 1-selected (Pharmacata) intNA public, Floorescently labelled CDNA was prepared from intNA, by oligiod 1-princed polymeration using SuperScript II reverse transcriptase IET Inc.). The proof of meteorides in the labelling resetion was 0.5 mM dCTP, dATP and dCTP and 0.2 mM dTTP. Fluorescent meteorides Rhodamire (in dCTP) (Perkin Elmer Cetus) or Cs3 dCTP (Amersham), were present at 0.1 mM, Pinkes were practiced by gel chromatography (BioSpin 6/BioRad) and ethanol precipitation.

Selection of CDNA elements and generation of control templates. Southers cDNAs were prepared by cloning random BunHI and HualIII ended tragments of E. off DNA in the very pSPed job (A)\* (Fromega), linearizing isolated plasmid DNA with Ecold and southesting pid) (A)\* (Isolat RNA competentiary to the insert from the resident SN6 promoter Chounga). From to use, the vintesced RNAs were selected on digit of redulines. The largest group of CDNAs consisted of 674 close CDNAs clones from the TSRI arrayed normalized infant brain brain. These commences were designed to the control of the CDNAs clones that cortesponded to a named gene according their members that cortesponded to a named gene according their members that cortesponded to a named gene according







Collagenase





Antichymotrypsin



Fig. 3 Nonnern hybridization substantialing the consistency of the cDNA microarray results. Corresponding locations within the cDNA microarray illustrated in Fig. 2a are provided for 1) Wal-1/p21; 2) MARCKS: 3) collagenase: 4) MCAF/MCP-1; 5) n-1antichymotrypsin: and 6) B-actin. The signal detected by a radio-labelled B-actin probe represents a control for loading vanance, with a red/green ratio observed on the cDNA microarray (Fig. 2a,c) for Bactin of 1 04

to the UniGene EST clustering system<sup>21,22</sup>. The second largest group of clones consisted of 183 sequenced cDNA clones generated by subtraction of cDNA from the chromosome-6 suppressed non-tumorigenic UACC-903 (+6) cell line with cDNA from its parental tumorigenic cell line UACC-903 (ref. 9). Approximately 100 additional genes (total 870 genes arrayed) were obtained from EST libraries on the basis of their expression pattern (tissue specific, and so on). Each array included the following hehridization controls: plasmid vector, lambda, 6X174 phage, total human DNA. human Cutl DNA, and poly (A)\*. The synthetic standards used for normalization of signals in each wavelength were also arrayed. Controls were included in

each quadrant of the array to assess the reproducibility of the hebridization signal. Two plates of cDNA clones (derived from the UACC-903 subtracted library) were also arrayed in duplicate. Fidelity of the Unigene array relative to dbEST was tested by sequencing of a random sample of 11 clones used for microarray construction. All sequences were identical with the Received 15 October, accepted 8 November, 1996.

corresponding dbl-ST emries. Additionally, each microarcayed cDNA from the UACC-903 subtracted library was sequenced. A listing of cDNAs comprising this microarray which were derived from the Unigene and 'housekeeping' panel can be obtained from http://www.nih.gov/DIR/LCG/ARRAY-expir-

Northern blot analysis, Total RNA, 10 µg per lane, was electrophoresed in 1,2% agarose-formaldehyde gels and transferred onto relon membrane (Hybond-N\*, Amersham) by capillary blotting overnight. For DNA probes insert fragments from the Soares INIB cDNA library to were obtained by vector PCR for p21, MARCKS, te-1-antichymotrypsin and B-actin. Probes for fibroblast collagenase and MCAF/MCP-1 were isolated from a UACC-903(+6) enriched cDNA library with all probes labelled by random priming. Filters were washed to a stringency of 0.1x SSC at 42 °C for 20 min.

Web sites, http://emgm.stanford.edu/pbrown for protocols and parts list pertaining to microarray tabrication. http://www.nchgr.pih.gov/DIR/LCG/ARRAY/expn.html for a listing of cDNAs comprising this microarray which were derived from the Unigene and housekeeping panel,

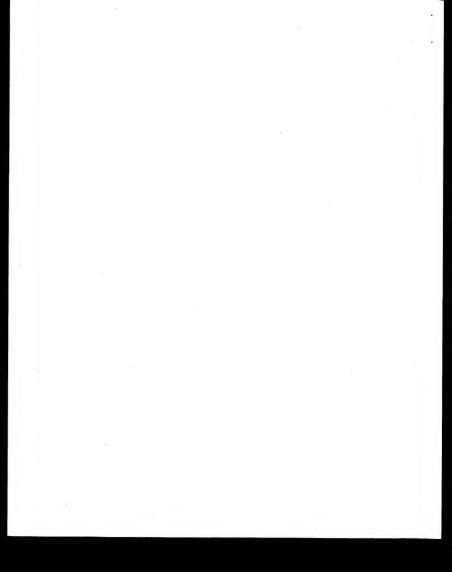
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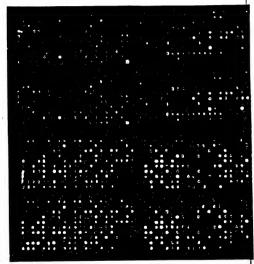
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### RESEARCH PAPERS

| Gene Transfer into Corn Earworm<br>(Helicoverpa 2ea) Embryos   | James D. DeVault, Keith J. Hughes,<br>Roger A. Leopold, Odell A. Johnson,<br>and Sudhir K. Narang                                    | 571 |
|--|--|-----|
| Identity-by-descent Mapping of Recessive Traits<br>in Livestock: Application to Map the Bovine<br>Syndactyly Locus to Chromosome IS                        | Carole Charlier, Frédéric Farnir,<br>Paulette Berzi,<br>Pascal Vanmanshoven,<br>Benoît Brouwers, Hans Vromans,<br>and Michel Georges | 580 |
| Sequencing the 500-kb GC-rich Symbiotic<br>Replicon of <i>Rhizobium</i> sp. NGR234 Using Dye<br>Terminators and a Thermostable "Sequenase":<br>A Beginning | Christoph Freiberg, Xavier Perret,<br>William J. Broughton, and<br>André Rosenthal   | 590 |
| Worldwide Distribution of Human<br>Y-chromosome Haplotypes   | Fabrício R. Santos,<br>Néstor O. Bianchi, and<br>Sérgio D.J. Pena  | 601 |
| Bacterial Artificial Chromosome Cloning and<br>Mapping of a 630-kb Human<br>Extrachromosomal Structure   | Min Wang, Stephanie Shouse,<br>Barbara Lipes, Ung-Jin Kim,<br>Hiroaki Shizuya, and Eric Lai  | 612 |
| LETTERS  |  |     |
| The Genomic Structure of Discoidin Receptor<br>Tyrosine Kinase   | Martin P. Playford, Robin J. Butler,<br>Xiao Cun Wang, Roy M. Katso,<br>Inez E. Cooke, and<br>Trivadi S. Ganesan                     | 620 |
| A Contiguous High-resolution Radiation Hybrid<br>Map of 44 Loci from the Distal Portion of the<br>Long Arm of Human Chromosome 5                           | Janet A. Warrington and<br>John J. Wasmuth   | 628 |
|  |  |     |

### GENOME METHODS

| Uniform Amplification of a Mixture of<br>Deoxyribonucleic Acids with Varying<br>GC Content                      | Namadev Baskaran,<br>Rajendra P. Kandpal,<br>Ajay K. Bhargava,<br>Michael W. Glynn, Allen Bale, and<br>Sherman M. Weissmann | 63  |
|---|---|-----|
| A DNA Microarray System for Analyzing<br>Complex DNA Samples Using Two-color<br>Fluorescent Probe Hybridization | Dari Shalon, Stephen J. Smith, and<br>Patrick O. Brown  | 639 |
| Microsatellite Hybrid Capture Technique for<br>Simultaneous Isolation of Various STR Markers                    | Michal Prochazka  | 646 |
| Erratum   |   | 650 |
| Product News  |   | 651 |

COVER DNA microarrays for analyzing complex DNA samples. Shown is a two-color fluorescent scan of an 1.8-cm  $\times$  1.8-cm yeast array of  $\lambda$  clones of yeast genomic DNA. (For details, see Shalon et al., p. 639.)

### A DNA Microarray System for Analyzing Complex DNA Samples Using Two-color Fluorescent Probe Hybridization

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Detecting and determining the relative abundance of diverse individual sequences in complex DNA samples is a recurring experimental challenge in analyzing genomes. We describe a general experimental approach to this problem, using microscopic arrays of DNA fragments on glass substrates for differential hybridization analysis of fluorescently labeled DNA samples. To test the system, 864 physically mapped \( \lambda \) clones of yeast genomic DNA, together representing >75% of the yeast genome, were arranged into l.8-cm × l.8-cm arrays, each containing a total of 1744 elements. The microarrays were characterized by simultaneous hybridization of two different sets of isolated yeast chromosomes labeled with two different fluorophores. A laser fluorescent scanner was used to detect the hybridization signals from the two fluorophores. The results demonstrate the utility of DNA microarrays in the analysis of complex DNA samples. This system should find numerous applications in genome-wide genetic mapping, physical mapping, and gene expression studies.

Many problems in genome analysis depend on determining what specific sequences are represented in a complex DNA or RNA sample and at what abundance, for example, what genes are represented in a specific chromosome band or YAC clone, what intervals are amplified or deleted in a particular cancer cell, or what genes are expressed in specific cells under specific conditions. As a general approach to this problem, we have developed a system for making microarrays of DNA samples on glass substrates, probing them by hybridization with complex fluorescentlabeled probes, and using a laser-scanning microscope to detect the fluorescent signals representing hybridization. Fluorescent labeling allows for simultaneous hybridization and separate detection of the hybridization signal from two or more probes. This in turn allows very accurate and reliable measurement of the relative abundance of specific sequences in two complex samples.

### RESULTS

### Array Hybridization Pattern

Figure 1 shows the two-color fluorescent scan of a veast genomic array following hybridization

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with a mixed probe consisting of lissaminelabeled DNA from the 6 largest yeast chromosomes together with fluorescein-labeled DNA from the 10 smallest yeast chromosomes. A red color indicates that yeast sequences present in the lissamine-labeled hybridization probe hybridized to an array element. A vellow-green color indicates that yeast sequences present in the fluorescein-labeled hybridization probe hybridized to an array element. An orange color indicates cross-hybridization of both chromosome pools to an array element (e.g., dispersed repetitive elements, such as Ty1 elements).

Each clone was spotted twice, resulting in duplicate hybridization patterns in adjacent quadrants of the array. Control DNA spots, which were randomly amplified in the same manner as the A clone array elements, are located in the bottom corner of each quadrant. "A" points to a pair of spots containing total yeast genomic DNA. These spots appear orange because both chromosome pools hybridized to yeast genomic DNA. The negative controls are as follows: "B" points to a pair of spots of wild-type  $\lambda$  DNA, "C" points to a pair of human genomic DNA spots, and "D" points to a pair of \$\phi X174 DNA spots. The lack of a hybridization signal at these three negative control spots indicates that the hybridization was specific for yeast sequences.

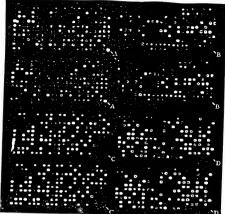


Figure 1 Two-color fluorescent scan of a 1.8-cm  $\times$  1.8-cm yeast array of  $\lambda$  clones of yeast genomic DNA. The DNA spots are spaced at a distance of 380  $\mu$ m from center to center. A probe mixture consisting of DNA from the 6 largest yeast chromosomes (4, 7, 12, 13, 15, 16) labeled with lissamine (red dots) and DNA from the 10 smallest yeast chromosomes (1, 2, 3, 5, 6, 8, 9, 10, 11, 14) labeled with fluorescein (yellow-green dots) was hybridized to the array. A pair of yeast genomic DNA spots (4) served as a positive control. The three negative controls are  $\lambda$  DNA (8), human genomic DNA (C), and  $\delta$ XT74 DNA (D).

### Karyotype Depiction of the Array Hybridization Pattern

The inserts contained in the arrayed  $\lambda$  clones have been mapped physically (Riles et al. 1993). The clones are arrayed in a random but known order on the array. Therefore, using the identity of each clone along with its physical map information, the pattern of hybridization to the yeast array can be represented in the form of a karyotype of the yeast genome, as shown in Figure 2. The color of any segment of the ideogram representing an individual chromosome on the karyotype is directly determined by the ratio of red and green hybridization signals at the array positions of the corresponding clones. The lengths of the discrete colored segments of each chromosome correspond to the physical lengths of the yeast

inserts. The chromosome segments colored black represent elther intervals of the genome that are not represented by clones in the library (90%) or false-negative hybridization signals on the array (10%). Most of these false negatives are attributable to failures of the PCR amplification of the  $\lambda$ clones, though occasional failures of the arraying process or nonuniform surface preparation could account for a small fraction of the false-negative signals. The large gap on chromosome 12 is the region coding for ribosomal DNA that was not represented among the arraved clones. Genomic intervals represented by overlapping clones were assigned a color based on the hybridization signals of only one of the overlapping clones, chosen at random.

Note that in this representation of a yeast karyotype, the largest six chromosomes are mainly colored red. This indicates that most of the arrayed clones that were mapped previously to these six large chromosomes hybridized primarily to the lissamine-labeled probe prepared from the corresponding purified chromosomes. Conversely, the smallest 10 chromosomes are mainly colored green in this image, matching the original CHET set inches

nal CHEF gel isolation of the chromosomes used as the hybridization probe. The experiment was repeated with the yeast genome split into six discrete chromosome pools containing 2—i chromosomes per pool using CHEF gel electrophoresis. The chromosomes in each pool were extracted from the gel, amplified, and fluorescently labeled. The six chromosome pools were hybridized to six separate yeast arrays. Forty-four \(\lambda\) clones gave a positive hybridization signal on all six arrays indicating that they contain yeast repetitive sequences (data not shown). These 44 clones and 10 clones with very weak hybridization signals were not included in the data set used to produce this karyotype.

There were -40 anomalous clones, which appear in this karyotype representation as green bands on the otherwise red chromosomes or red

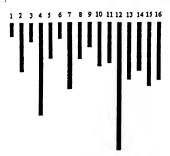


Figure 2 Computer-generated ideogram representing a karyotype of 5 cerevisize, based on the normalized hybridization signals from the array shown in Fig. 1. Note that the 6 largest chromosomes are mainly red and the 10 smallest chromosomes are mainly green. Black stripes represent intervals not represented by clones in the array or for which the corresponding clones gave false-negative hybridization signals.

bands on the otherwise green chromosomes. Four randomly chosen examples of these anomalous clones were analyzed by hybridizing the clones to vertical strips cut from a Southern blot of CHEF gel-separated yeast chromosomes. In each case, the hybridization patterns of the anomalous clones corroborated the chromosomal locations assigned by the microarray hybridization results (data not shown). Two clones that were thought to map to the 10 smallest chromosomes were found to hybridize preferentially to the probe representing the 6 largest chromosomes and thus appear as anomalous red bands on the karvotype. Both hybridized to one of the six largest chromosomes on the Southern blot. Similarly, two clones that appear as anomalous green bands on the karvotype were found to hybridize to one of the 10 smallest chromosomes on the Southern blot. Thus, the anomalous clones are probably the result of sample tracking errors or, possibly, of errors in the published restrictiondigest-based physical map on which the karvotype representation was based (Riles et al. 1993).

### DISCUSSION

The DNA microarray hybridization system reported here is conceptually and functionally

similar to fluorescent in situ hybridization (FISH) to metaphase chromosomes, with three important differences. First, the target elements of the microarrays can, in principle, be any length or composition, from megabase YAC clones or microdissected chromosome bands to individual cDNA clones, to short oligonucleotides. This versatility allows the user to choose characteristics. such as the mapping resolution and genetic complexity of each array element, to suit a particular application. Second, the hybridization signals are localized to discrete elements of known size and location, making them easier to identify and quantitate than the hybridization signals from irregularly shaped metaphase spreads. Third, microarrays are more consistent and potentially amenable to automated production, hybridization, and data analysis than metaphase spreads.

Arrays of DNA samples on porous membranes, for example, dot blots, have long been used as a basic tool in molecular biology. Dotblot membranes are usually at least 8 × 12 cm in size, require the use of milliliter volumes of hybridization solution, and are limited, owing to autofluorescence and scattering, to radioactive. chemiluminescent, and colorimetric hybridization detection methods (Ross et al. 1992). Microarrays made on glass surfaces, on the other hand, can be mass-produced and are comparatively inexpensive, convenient, and compatible with fluorescent hybridization detection methods. Furthermore, a glass surface, when appropriately treated, has very low nonspecific binding of labeled hybridization probes, resulting in lower backgrounds than are encountered typically with porous membranes. For hybridizations with very complex probes, the concentration of the labeled probe DNA is a limiting factor in the sensitivity of the assay. Minimizing the volume of the probe solution in a hybridization, by restricting the target to a small area and by using a nonporous substrate, makes it practical to achieve very high probe concentrations.

One important advantage of fluorescently labeled probes is that, unlike most radioactive and chemiluminescent signals, fluorescent signals do not disperse and therefore allow for very dense array spacing. A unique, and probably the most important, advantage of fluorescent probes is that the hybridization signals from two or more differently labeled probes hybridized to the same target element can be detected separately. In this way, two-color hybridization detection allows for a direct and quantitative comparison of the

abundance of specific sequences between two probe mixtures that are hybridized competitively to a single array. The absolute intensity of a hybridization signal at a particular element in an array can vary owing to experimental factors such as variations in the amount of DNA deposited on the array, variations in the hybridization or wash conditions between experiments, or variations in the hybridization characteristics of the different DNA sequences on the array. The ratio of the two signals at any element in an array, however, is relatively insensitive to these confounding factors because they affect both probe mixtures equivalently. This ratio therefore accurately reflects the relative abundance of the cognate sequence in the two probe samples. This is the principle underlying the technique of comparative genomic hybridization (CGH), which is used to detect changes in the copy number of specific chromosomes or chromosomal regions (Kallioniemi et al. 1992). CGH is based on measuring the relative fluorescent hybridization intensities of two genomic-complexity hybridization probes, for example, probes representing genomic DNA from normal and affected tissue samples, which are labeled with two distinct fluorophores and hybridized simultaneously to a metaphase spread. DNA microarray representations of the human genome may provide a more convenient and higher resolution alternative to metaphase chromosomes for CGH.

Cross-hybridization between related sequences is an important problem faced by any hybridization-based assay, including the DNA microarray assay described here. Studies are now in progress to quantitate the extent of cross-hybridization between related sequences of varying homology and length, in DNA microarray hybridizations. The stringency of hybridization and washing can be controlled by varying the salt concentration and temperature as in convenient in the controlled by the concentration and temperature as in convenient in the controlled by t

Alternative methods have been described for making microarrays of very short DNA sequences, involving photolithography (Pease et al. 1994) or physical masking (Maskos and Southern 1992) methods. These in situ synthesis methods are inherently limited to low complexity array elements consisting of oligonucleotides. For complex-probe hybridizations, the specificity of

hybridization is improved by using DNA fragments substantially longer than oligonucleotides. Moreover, the in situ synthesis approaches to array fabrication depend on prior knowledge of the sequence to be recognized by each array element. The approach described here makes microarrays by transferring tiny volumes of DNA samples from microwell storage plates to a solid substrate. Thus, nucleic acids (or other molecules) of virtually any length or any origin can be arrayed, and knowledge of their sequences is not required.

The arrays used in these experiments do not represent the maximal achievable density of elements. We have found that the spacing between the spots can be decreased by shrinking the contact area of the printing tip and by increasing the hydrophobicity of the glass surface. Microarrays with 100-um feature size have been tested successfully in pilot experiments (data not shown). Assuming the projected availability of the appropriate physically mapped human genomic clones (Hudson et al. 1995), arravs at 100-um spacing would allow for 10,000 discrete intervals of the human genome to be represented in a 1-cm<sup>2</sup> array. Such an array could be used for mapping at a resolution of <0.5 Mb. Experiments are in progress to explore the feasibility of such arrays.

Our initial motivation for developing these microarrays arose from the need for abundant and inexpensive genomic arrays for genomic mismatch scanning (GMS) (Nelson et al. 1993), a method of genetic linkage analysis based on identification of the regions of "identity by descent" between affected relative pairs using a single complex-probe hybridization to an array of genomic clones. Experiments using these arrays to map quantitative trait loci in yeast by GMS are currently in progress J. deRisi, D. Lashkari, L. Penland, L. McAllister, J. McCusker, R. Davis, and P.O. Brown, unpubl.).

Microarrays of cDNA clones, prepared using the system described here, have been used for quantitative monitoring of gene expression patterns in Arabidopsis (Schena et al. 1995), S. cerevisiae (D. Lashkari, J. deRisi, L. Penland, P.O. Brown, and R. Davis, unpubl.), and human tissues (J. deRisi, M. Bittner, P. Meltzer, L. Penland, J. Trent, and and P.O. Brown, unpubl.). We anticipate that DNA microarrays of the kind described here will be useful in additional applications for which conventional dot blots, high-density gridded arrays on porous membranes, or FISH are currently used. These potential applica-

tions include comparative genomic hybridization (Kallioniemi et al. 1992), sequencing by hybridization (Drmanac et al. 1993), physical mapping of cloned or amplified sequences (Billings et al. 1991), and economical distribution of reagents for integrated genetic and physical mapping based on a common set of arrayed clones (Zehetner and Lehrach 1994).

### METHODS

### Amplification of Target DNA Elements

The array elements were prepared from physically mapped A clones (Riles et al. 1993). The A clones were amplified using randomly primed polymerase chain reaction (PCR) based on published and unpublished protocols (Bohlander et al. 1992; S. Nelson, unpubl.). The phage lysates were amplified in a 10-µl PCR reaction using 5 µM final concentration of primer A (GCTATCTTCAAGATCANNNNNN), 200 um dNTPs, and 1 unit of Tag polymerase. Round A consisted of five cycles at 94°C for 1 min, 25°C for 1.5 min, 25-72°C over 7 min, and 72°C for 3 min using Tag polymerase (BMB). For round B, the reaction volume was brought up to 100 µl for a final concentration of 2 µm of primer B (GCTATCTTCAAGATCA), 200 µm dNTPs, and 4 units of Tag polymerase. Round B consisted of 30 cycles of 94°C for 1 min, 56°C for 2 min, and 72°C for 3 min. The amplification was performed in 96-well plates using crude phage lysates as the templates, resulting in an amplification of both the 35-kb & vector and the 5-kb to 15-kb yeast insert sequences as a distribution of PCR products between 250 bp and 1500 bp in length.

The PCR products were purified and transferred into TE (10 mm Tns, 1 mm EDTA at pH 8.0) buffer using Sephadex G50 gei filtration (Pharmacia) and evaporated to dryness at room temperature overnight. Each of the 864 am

plified  $\lambda$  clones was rehydrated in 15  $\mu$ l of 3 $\times$  SSC (20 $\times$  SSC = 3  $\times$  NaCl. 0.3  $\times$  Na<sub>3</sub> citrate) in preparation for sporting onto the glass under normal room temperature conditions.

### Preparation of DNA Microarrays

The microarrays were fabricated on poly-i-lysine coated microscope slides (Sigma). A custom-built arraying machine, consisting of four tweezer-like printing tips mounted 9 mm apart on a computer-controlled robotic stage (Shalon 1996), loaded 1 µl of the concentrated PCR product directly from corresponding clusters of four wells of 96-well storage plates and deposited -5 nl of each sample onto each of 40 slides. Surface tension loaded the sample into the printing tip directly from the microwell plate and held the sample in the tip during the printing operation. Printing was achieved by lightly tapping the tip against the glass surface. The open-capillary design allowed for rapid nasing and drving of the tips between samples. Figure 3 shows the layout of the arraving machine. Figure 4 shows a detailed view of the four printing tips and the staggered printing pattern on the microscope slides. Adjacent samples were spotted 380 um apart on the slides. After each set of four samples was printed onto 40 slides, the printing tips were rinsed with a jet of water for 2 sec and then dried by lowering the tips onto a sponge for 2 sec. The process was repeated for all 864 samples and eight control spots.

After the sporting operation was complete, the slides were rehydrated in a humid chamber at room temperature for 2 hr. baked in an 80°C vacuum oven for 2 hr, then nined in 0.1% sodium doderyl sulfatte (SDS) to remove unadsorbed DNA. To reduce nonspecific adsorption of the labeled hybridization probe to the poly-t-lysine coated glass surface the slides were treated with succinic anhydride. One gram of succinic anhydride was dissolved in 100 mil of 1 methyl-2-pyriopidingone and then 100 mil of 1 methyl-2-pyriopidingone.

0.2 w boric acid (pH 8.0) was added. The arrays were soaked in this solution for 10 min and then rinsed in distilled water four times for 5 min each. Immediately before use, the arrayed DNAelements were denatured by placing the slide in distilled water at 90°C for 2 min.

# Printhead motion Baseplate Microwell plates Microscope slides

Figure 3 The layout of the arraying machine. All motions are under computer control. For more details of the arraying machine, see web page http://cmpm.stanford.edu/obrown.

### Amplification and Labeling of Hybridization Probe

The 16 chromosomes of Saccharomics cerevisuae were separated using a contous-clamped homogeneous electric field (CHEF) agarose gel apparatus (Bio-Rad) (Lot et al. 1986). The 6 largest chromosomes were isolated in one gel since and the smallest ten chromosomes in a second gel slice. The DNA from each slice was recovered using a gel extraction kit

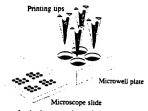


Figure 4 A close-up view of the four opencapillary printing tips. The tips are 9 mm apart and fit into four adjacent wells of a standard microwell plate and print arrays in a staggered fashion on microscope slides. For more details of the printing tips, see web page http://cmm.stanford.edu/pbrown.

(Giagen) and randomly amplified in a manner similar to that used in amplifying the target \( \) clones (Grothues et al. 1993). The main difference between this amplification procedure and the one used for the \( \) array elements is a filtration step between rounds \( \) and a first enemoey primer-dimers and the use of a random 9-mer \( \) are of on primer \( \) A following amplification. \( \) 25 \( \) gof et ach for the amplified chromosome pools were separately random-primer labeled using \( \) (for each polymeras (Ameriham) with a lissamine-conjugated nucleotide analog (DuPont NEN) for the pool containing the foliagest chromosomes and with a fluorescent-conjugated nucleotide analog (BMB) for the pool containing the smallest 10 chromosomes. The two fluorescent-labeled pools were mixed and concentrated using an uttrafitization device (Ameroli).

### Hybridization

Five micrograms of the hybridization probe, consisting of both chromosome pools in 7.5 µl of TE, was denarured in a boiling water bath and then snap-cooled on ice. Concentrated hybridization solution (2.5 µl) was added to a final concentration of 5 × SSC/0.1% SDS. The entire 10 µl of probe solution was transferred to the array surface, covered with a coverslip, placed in a custom-built single-slide humidity chamber, and incubated in a 60°C water bath for 12 hr. The custom-built waterproof slide chamber has a cavity just slightly bigger than a microscope slide and was kept at 100% humidity internally by the addition of 2 µl of water in a corner of the chamber. The slide was rinsed in 5x SSC/0.1% SDS for 5 min and then in 0.2× SSC/0.1% SDS for 5 min. All rinses were at room temperature. The array was then air dried, and a drop of antifade (Molecular Probes) was applied to the array under a 24-mm  $\times$  30-mm coverslip in preparation for scanning.

### Detection and Analysis

A custom-built laser scanner was used to detect the two-

color fluorescence hybridization signals from 1.8cm × 1.8-cm arrays at 20-µm resolution. The glass substrate slide was mounted on a computer-controlled, twoaxis translation stage (PM-500, Newport, Irvine, CA) that scanned the array over an upward-facing microscope objective (20 x , 0.75NA Fluor, Nikon, Melville, NY) in a bidirectional raster pattern. A water-cooled Argon/Krypton laser (Innova 70 Spectrum, Coherent, Palo Alto, CA), operated in multiline mode, allowed for simultaneous specimen illumination at 488.0 nm and 568.2 nm. These two lines were isolated by a 488/568 dual-band excitation filter (Chroma Technology, Brattleboro, VT). An epifluorescence configuration with a dual-band 488/568 primary beam splitter (Chroma) excited both fluorophores simultaneously and directed fluorescence emissions toward the two-channel detector. Emissions were split by a secondary dichroic mirror with a \$65 transition wavelength onto two multialkali cathode photomultiplier tubes (PMT; R928, Hamamatsu, Bridgewater, NJ), one with an HQ\$35/50 bandpass barrier filter and the other with a D630/60 bandpass barrier filter (Chroma). Preamplified PMT signals were read into a personal computer using a 12-bit analog-todigital conversion board (RTI-834, Analog Devices, Norwood, MA), displayed in a graphics window, and stored to disk for further rendering and analysis. The back aperture of the 20× objective was deliberately underfilled by the illuminating laser beam to produce a large-diameter illuminating spot at the specimen (5-µm to 10-µm halfwidth). Stage scanning velocity was 100 mm/sec, and PMT signals were digitized at 100 µsec intervals. Two successive readings were summed for each pixel, such that pixel spacing in the final image was 20 µm. Beam power at the specimen was -5 mW for each of the two lines.

The scanned image was despeckled using a graphics promain Hijiaak Praphics Suitel and then analyzed using a custom image graphics Suitel and then analyzed using a custom image grading program that created a spread-sheet of the average red and green hybridization intensities for each spot. The red and green hybridization intensities were corrected for optical cross talk between the fluorescein and lissamine channels, using experimentally determined coefficients.

### **ACKNOWLEDGMENTS**

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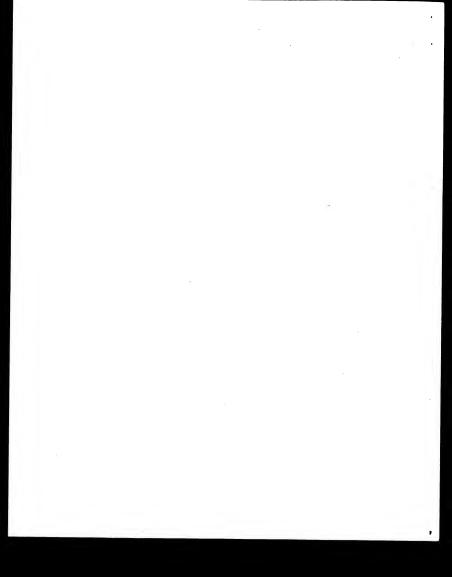
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### Discovery and analysis of inflammatory disease-related genes using cDNA microarrays

(inflammation/buman genome analysis/gene discovery)

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Contributed by Ronald W. Davis, December 27, 1996

cDNA microarray technology is used to profile complex diseases and discover novel disease-related genes. In inflammatory disease such as rheumatoid arthritis, expression patterns of diverse cell types contribute to the pathology. We have monitored gene expression in this disease state with a microarray of selected human genes of probable significance in inflammation as well as with genes expressed in peripheral human blood cells. Messenger RNA from cultured macrophages, chondrocyte cell lines, primary chondrocytes, and synoviocytes provided expression profiles for the selected cytokines, chemokines, DNA binding proteins, and matrix-degrading metalloproteinases. Comparisons between tissue samples of rheumatoid arthritis and inflammatory bowel disease verified the involvement of many genes and revealed novel participation of the cytokine interleukin 3, chemokine Grow and the metalloproteinase matrix metallo-elastase in both diseases. From the peripheral blood library, tissue inhibitor of metalloproteinase 1. ferritin light chain, and manganese superoxide dismutase genes were identified as expressed differentially in rheumatoid arthritis compared with inflammatory bowel disease. These results successfully demonstrate the use of the cDNA microarray system as a general approach for dissecting human diseases.

The recently described CDNA microarray or DNA-chip technology allows expression monitoring of hundreds and thousands of genes simultaneously and provides a format for identifying gene sa well as changes in their activity (1, 2). Using this technology, two-color fluorescence patterns of differential gene expression in the root versus the shoot tissue of Arabidoptis were obtained in a specific array of 48 genes (1). In another study using a 1000 gene array from a human peripheral biood library, novel genes expressed by T cells were identified upon heat shock and proprien kinase Cacitivation (3).

The technology uses cDNA sequences or cDNA inserts of a library for PCR amplification that are arrayed on a glast side with high speed robotics at a density of 1000 cDNA sequences per cm<sup>2</sup>. These microarrays serve as gene tagget for hybridization to cDNA probes prepared from RNA samples of cells or tissues. A two-color fluorescence labeling technique is used in the preparation of the cDNA probes such that a simultaneous hybridization but separate detection of signals provides the comparative analysis and the relative abundance of specific genes expressed (1, 2) Microarrays can be constructed from specific cDNA clones of interest, a cDNA library, or a select number of open reading frames from a genome sequencing database to allow a large-scale functional analysis of expressed sequences.

significance in RA were identified. Regions of the clones, preferably lkb in length, were selected by their proximity to the 3 end of the cDNA and for areas of least identity to related and repetitor sequences. Primer were synthesized to amplify the target regions by standard PCR protocols (3). Products were Abbreviations: RA, rheumatoid arthritis; MMP, matrix-degrading metalloproteinase; IBD, inflammatory bowel disease; IPS, improblematical and the control of the co

Because of the wide spectrum of genes and endogenous

mediators involved, the microarray technology is well suited

for analyzing chronic diseases. In rheumatoid arthritis (RA),

inflammation of the joint is caused by the gene products of

many different cell types present in the synovium and cartilage

tissues plus those infiltrating from the circulating blood. The autoimmune and inflammatory nature of the disease is a

cumulative result of genetic susceptibility factors and multiple responses, paracrine and autocrine in nature, from macro-

phages. T cells, plasma cells, neutrophils, synovial fibroblasts,

chondrocytes, etc. Growth factors, inflammatory cytokines (4), and the chemokines (5) are the important mediators of this

inflammatory process. The ensuing destruction of the cartilage

and bone by the invading synovial tissue includes the actions

of prostaglandins and leukotrienes (6), and the matrix degrading metalloproteinases (MMPs). The MMPs are an important

class of Zn-dependent metallo-endoproteinases that can col-

lectively degrade the proteoglycan and collagen components of

select classes of molecules in RA was examined. Also inves-

tigated were 1000 human genes randomly selected from a

peripheral human blood cell library. Their differential and quantitative expression analysis in cells of the joint tissue, in

diseased RA tissue and in inflammatory bowel disease (IBD)

tissues was conducted to demonstrate the utility of the mi-

croarray method to analyze complex diseases by their pattern

of gene expression. Such a survey provides insight not only into

the underlying cause of the pathology, but also provides the

opportunity to selectively target genes for disease intervention

METHODS

Microarray Design, Development, and Preparation. Two ap-

proaches for the fabrication of cDNA microarrays were used in

this study. In the first approach, known human genes of probable

by appropriate drug development and gene therapies.

This paper presents a study in which the involvement of

the connective tissue matrix (7).

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T cell expressed and secreted; Gel, gelatinase; V.A.M., vascular cell addesion molecule; ICE. IL-l converting enzyme; PUMP, putative metalloproteinase; MnSOD, manganese superoxide dismutate; TIMP, tissue inhibitor of metalloproteinase; MCP, macrophage chemotactic protein.

protein.
To whom reprint requests should be sent at the present address:
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verified by gel electrophoresis and purified with Oiaquick 96-well purification kit (Qiagen, Chatsworth, CA), Ivophilized (Savant). and resuspended in 5 µl of 3× standard saline citrate (SSC) buffer for arraying. In the second approach, the microarray containing the 1056 human genes from the peripheral blood lymphocyte library was prepared as described (3).

Tissue Specimens. Rheumatoid synovial tissue was obtained from patients with late stage classic RA undergoing remedial synovectomy or arthroplasty of the knee. Synovial tissue was separated from any associated connective tissue or fat. One gram of each synovial specimen was subjected to RNA extraction within 40 min of surgical excision, or explants were cultured in serum-free medium to examine any changes under in vitro conditions. For IBD, specimens of macroscopically inflamed lower intestinal mucosa were obtained from patients with Crohn disease undergoing remedial surgery. The hypertrophied mucosal tissue was separated from underlying connective tissue and extracted for RNA.

Cultured Cells. The Mono Mac-6 (MM6) monocytic cells (8) were grown in RPMI medium. Human chondrosarcoma SW1353 cells, primary human chondrocytes, and synoviocytes (9. 10) were cultured in DMEM; all culture media were supplemented with 10% fetal bovine serum, 100 µg/ml streptomycin, and 500 units/ml penicillin. Treatment of cells with lipopolysaccharide (LPS) endotoxin at 30 ng/ml, phorbol 12-myristate 13-acetate (PMA) at 50 ng/ml, tumor necrosis factor α (TNF-α) at 50 ng/ml, interleukin (IL)-1β at 30 ng/ml, or transforming growth factor-\(\beta\) (TGF-\(\beta\)) at 100 ng/ml is described in the figure legends.

Fluorescent Probe, Hybridization, and Scanning. Isolation of mRNA, probe preparation, and quantitation with Arabidopsis control mRNAs was essentially as described (3) except for the following minor modification. Following the reverse transcript ase step, the appropriate Cy3- and Cy5-labeled samples were pooled: mRNA degraded by heating the sample to 65°C for 10 min with the addition of 5 µl of 0.5M NaOH plus 0.5 ml of 10 mM EDTA. The pooled cDNA was purified from unincorporated nucleotides by gel filtration in Centri-spin columns (Princeton Separations, Adelphia, NJ). Samples were ivophilized and dissolved in 6 µl of hybridization buffer (5× SSC plus 0.2% SDS). Hybridizations washes, scanning, quantitation procedures, and pseudocolor representations of fluorescent images have been described (3). Scans for the two fluorescent probes were normalized either to the fluorescence intensity of Arabidopsis mRNAs spiked into the labeling reactions (see Figs. 2-4) or to the signal intensity of β-actin and glyceraldehyde-3-phosphate dehydrogenase (GAPDH; see Fig. 5).

### RESULTS

Ninety-Six-Gene Microarray Design. The actions of cytokines. growth factors, chemokines, transcription factors, MMPs, prostaglandins, and leukotrienes are well recognized in inflammatory disease, particularly RA (11-14). Fig. 1 displays the selected genes for this study and also includes control cDNAs of housekeeping genes such as B-actin and GAPDH and genes from Arabidopsis for signal normalization and quantitation (row A, columns 1-12).

Defining Microarray Assay Conditions. Different lengths and concentrations of target DNA were tested by arraying PCR-

|      | 1               | 2                  | 3               | 4            | 5                         | 6                                      | 7               | 8                | 9                    | 10                              | 11                | 12            |
|------|-----------------|--------------------|-----------------|--------------|---------------------------|--|-----------------|------------------|----------------------|---------------------------------|-------------------|---------------|
| A    | BLANK           | BLANK              | HAT1<br>HAT1    | HAT1<br>HAT1 | HAT4<br>HAT4              | HAT4<br>HAT4                           | HAT22<br>HAT22  | HATZZ<br>HATZZ   | YESZ3<br>YESZ3       | YESZ3                           | BACTIN            | СЗРОН         |
| В    | IL1A<br>IL-1a   | IL1B<br>IL-1β      | IL1RA<br>IL-1RA | IL2<br>IL-2  | IL3<br>IL3                | E.4                                    | EL-6            | ILBR<br>IL-6R    | IL7<br>IL-7          | CFOS<br>c-fos                   | CJUN<br>c-jun     | RFRA1         |
| C    | ILB<br>IL-8     | IL-9               | IL10<br>IL-10   | ICE<br>ICE   | .IFNG<br>IFN <sub>f</sub> | GCSF<br>G-CSF                          | MCSF<br>M-CSF   | GMICSF<br>GM-CSF | TNFB.1               | CREL<br>c-rel                   | NFKB50<br>NFxBp50 | NFKB65        |
| D    | TNFA.1          | TNFA.2<br>TNFa     | TNFa.3          | TNFA.4       | TNFA.5                    | TNFRL1                                 | TNFRL2<br>TNFri | TNFF81.1         | TNFRIL2<br>TNFrii    | NFKB85.2<br>NFxBp65             | IKB<br>IdB        | CREB2         |
| =    | STR1<br>Strom-1 | STR2-3'<br>Strom-2 | Strom-3         | COL1         | COL1-3'                   | COL21<br>Col-2                         | COL22<br>Coll-2 | Col-3            | COX1                 | COX2<br>Coxe                    | 12L0<br>- 124.0   | 15L0<br>15-L0 |
| -    | GELA.1          | GELB<br>Gel-B      | HME<br>Bastase  | MT-MMP       | PUMP1<br>Matriysin        | TIMP1                                  | TIMP2           | TIMP3            | ICAM1                | VCAM<br>VCAM                    | 5LO.1<br>5-LO     | CPLAZ.2       |
| ŝ    | EGF .           | FGF acidic         | FGF besic       | IGPI<br>IGFI | IGFII                     | TGFA                                   | TGF8            | PDGF8            | CALCTN<br>Calcitonin | GH1                             | CRO<br>GRO1α      | GCR.          |
| 1    | MCP-1           | MCP-1              | MIP1A<br>MIP-1a | MP1B<br>MP1β | MF                        | RANTES<br>RANTES                       | INOS<br>INOS    | LDLA             | ALU.1                | ALU.2<br>TNFRp70                | ALU.3             | POLYA         |
| 1000 |                 | aliana controls    |                 | Trans        |                           | elated gen<br>ctors and r<br>ted genes |                 |                  | . Grow               | okines<br>In factors a<br>genes | ind related       | genes         |

Fig. 1. Ninety-six-element microarray design. The target element name and the corresponding gene are shown in the layout. Some ge more than one target element to guarantee specificity of signal. For TNF the targets represent decreasing lengths of 1, 0.8, 0.6, 0.4, and 0.2 kb from left to right.

amplified products ranging from 0.2 to 1.2 kb at concentrations of 1  $\mu g/\mu$  or less. No significant difference in the signal levels was observed within this range of target size and only with 0.2 ×b length was a signal reduced upon an 8-fold dilution of the 1  $\mu g/\mu$  sample (data not shown). In this study the average length of the targets was 1 kb, with a few exceptions in the range of -300 bp, arrayed at a concentration of 1  $\mu g/\mu$ l. Normally one PCR provided sufficient material to fabricate up to 1000 microarray targets.

In considering positional effects in the development of the targets for the microarray, selection was bisased toward the 3' proximal regions, because the signal was reduced if the target fragment was bisased toward the 5' end (data not shown). This result was anticipated since the hybridizing probe is prepared by revenes transcription with oligo(GT)-primed mRNA and is richer in 3' proximal sequences. Cross-hybridizations of probes to targets of a gene family were analyzed with the matrix metal-

loproteinasts at the example because they can show regions of sequence identities of greater than 70%. With collagenass-1 (Col-1) and collagenass-2 (Col-2) genes as targets with up to 70% sequence identity, and stromelyain-1 (Strom-1) and stromelyain-2 (Strom-2) genes with different degrees of identity, our results showed that a short region of overlap, even with 70-90% sequence identity, produced a low level of cross-hybridization. However, shorter regions of identity spread over the length of the target resulted in cross-hybridization (data not shown). For closely related genes, targets were designed by avoiding long stretches of homology. For members of a gene family two or more target regions were included to discriminate between specificity of signal versus cross-hybridization.

Monitoring Differential Expression in Cultured Cell Lines. In RA tissue, the monocyte/macrophage population plays a prominent role in phagocytic and immunomodulatory activities. Typ-

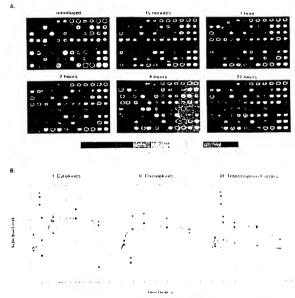


FIG. 2. Time course for LPS/PMA-induced MM6 cells. Array elements are described in Fig. 1. (4) Pseudocolor: epresentations of fluorescent scans correspond to gene expression levels at a tech time point. The array is made up of 8 Arabdopus control targets and 86 human CDNA targets, the majority of which are genes with known or suspected involvement in inflammation. The color barry provide a comparative calibration scale between arrays and are derived from the Arabdopsus mRNA samples that are introduced in equal amounts during probe preparation. Ploroscent probes were made by labeling mRNA from untreated MM6 cells or LPS and PMA treated cells: mRNA was soluted at a indicated times after induction. (B I-III) The two-color samples were cohybridized, and microarray scans provided the data for the levels of select transcripts at different time points relative to abundance at time zero. The analysis was performed using normalized data collected from 8-bit images.

ically these cells, when triggered by an immunogen, produce the proinflammatroy cytokines TNF and IL-1. We have used the monocyte cell line MM6 and monitored changes in gene expression upon activation with LPS endotoxin, a component of Gramnegative bacterial membranes, and PMA, which augments the action of LPS on TNF production (15). RNA was isolated at different times after induction and used for cDNA probe preparation. From this time course it was clear that TNF expression was induced within 15 min of treatment, reached maximum levels in 1 hr, remained high until 4 hr and subsequently declined (Fig. 24). Many other cytokine genes were also transiently activated. such as IL-1α and -β. IL-6, and granulocyte colony-stimulating factor (GCSF). Prominent chemokines activated were IL-8, macrophage inflammatory protein (MIP)-18, more so than MIP-1a. and Groa or melanoma growth stimulatory factor. Migration inhibitory factor (MIF) expressed in the uninduced state declined in LPS-activated cells. Of the immediate early genes, the noticeable ones were c-fos, fra-1, c-iun, NF-xBp50, and IxB with c.ml expression observed even in the uninduced state (Fig. 2B). These expression patterns are consistent with reported patterns of activation of certain LPS- and PMA-induced genes (12). Demonstrated here is the unique ability of this system to allow parallel visualization of a large number of gene activities over a period of time

SW1353 cells is a line derived from malignant tumors of the cartilage and behaves much like the chondrocytes upon stimulation with TNF and IL-1 in the expression of MMPs (9). In addition to confirming our earlier observations with Northern blots on Strom-1. Col-1, and Col-3 expression (9), gelatinase (Col-1), and col-3 expression (9), gelatinase (Col-1), and col-3 expression (9), generating the color of t

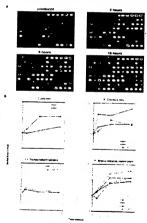


Fig. 3. Time course for IL-1β and TNF-induced SW1353 cells using the inflammation array (Fig. 1). (A) Pseudocolor representation of fluorescent seans correspond to gene expression levels at each time point. (B-I-IV) Relative levels of selected genes at different time points compared with time zero.

type matrix metalloproteinase, tissue inhibitors of matrix metalloproteinase or tissue inhibitor of metalloproteinase i (TIMP-1).-2, and -3 were also expressed by these cells together with the human matrix metallo-clastase (HME: Fig. 34). HME induction was estimated to be -95-fold and was greater than any of the other MMPs examined (Fig. 38). This result was unexpected because HME is reportedly expressed only by alveolar macrophage and placental cells (16). Expression of the cytokines and chemokines. I.-6, II.-8, MIF- and MIP-Ig was also noted. A variety of other genes, including certain transcription factors, were also up-regulated (Fig. 3), but the overall time-dependent expression of genes in the SWJ353 cells was qualitatively distinct from the MM6 cells.

Quantitation of differential gene represents (Figs. 28 and 38) was achieved with the semutaneous by modization of Cy3-labeled cDNA from untreated to by modization of Cy3-labeled cDNA from untreated camples. The estimated increases in expression from these microarrays for a select number of genes including IL-18, IL-8, IMP-18, TNF, IME. Col.1, Col.3. Strom-1, and Strom-2 were compared with data collected from dot blot analysis. Results (not shown) were in close agreement and confirmed our earlier observations on the use of the microarray method for the quantitation of gene expression (3).

Expression Profiles in Primary Chondrocytes and Synovices of Human RA Tissue. Given the sensitivity and the specificity of this method, expression profiles of primary ynoviocytes and chondrocytes from diseased issue were examined. Without prior exposure to inducing agents, low level expression of cjun. OCSF, IL-3, TNF-B, MIF. and RANTES (regulated upon activation, normal T cell expressed and seried) was seen as well as expression of MMPs, GelA, Strom-I, Col-I, and the three TIMPs. In this case, Col-2 hybridization was considered to be nonspecific because the second Col-2 target taken from the 3' end of the spece gave no

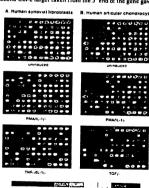


Fig. 4. Expression profiles for early passage primary provincytes and chondrocytes solated from RA issue, cultured in the presence of No, feal call serum and activated with PMA and IL-18, or TNF and IL-18, or TOF-\$61 tills. The color bars provide a comparaire calibration scale between arrays and are derived from the Archadoptus mRNA samples that are introduced in equal amounts during probe preparation.

signal. Treatment more to with PMA and IL-1, than TNF and IL-1, produced a dramatic up-regulation in expression of several genes in both of these primary cell types. These genes are as follows: the cytokine IL-6, the chemokines IL-8 and Gro-1e, and the MMPs. Strom-1, Col-1, Col-3, and HME, and the adhesion modesule, vaccular cell adhesion modesule. (VCAM-1). The surprise again is HME after the collection of the primary cells, for reason discussed above, From these intuits, the expression profiles of synovicoytes and the chondrocytes appear very similar; the differences are more quantitative than qualitative. Treatment of the primary chondrocytes with the anabolic growth factor TGF-8 had an interesting profile in that it produced a remarkable down-regulation of genes expressed in both the unreasted and induced state (Fig. 4).

Given the demonstrated effectiveness of this technology, a comparative analysis of two different inflammatory disease states was conducted with probes made from RA tissue and IBD samples. RA samples were from late stage rheumatoid synovial tissue, and IBD specimens were obtained from inflamed lower intestinal mucosa of patients with Crohn disease. With both the 96-element known gene microarray and the 1000-gene microarray of cDNAs selected from a peripheral human blood cell library (3), distinct differences in gene expression patterns were evident. On the 96-gene array, RA tissue samples from different affected individuals gave similar profiles (data not shown) as did different samples from the same individual (Fig. 5). These patterns were notably similar to those observed with primary synoviocytes and chondrocytes (Fig. 4). Included in the list of prominently up-regulated genes are IL-6, the MMPs Strom-1, Col-1, GelA, HME, and in

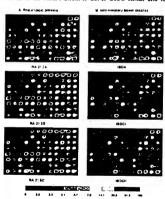


Fig. 5. Expression profiles of RA tissue (4) and IBD tissue (8), mRNA from RA tissue samples obtained from the same individual vasionated directly after excision (RA 21.54) or maintained in culture withous serum for 2 fr (RA 21.55) po for 6 for RA (21.5C). Profiles from tissue samples of two other individuals (data nos shown) were roundledly similar to the ones shown here. IBD-A and IBD-C1 are marked by similar to the ones shown here. IBD-A and IBD-C1 separate individuals. For the IBD-C11 probe, the tissue samples was considered in medium without serum for 2 for before mRNA preparation.

certain samples PUMP. TIMPs, particularly TIMP-1 and TIMP-3, and the adhesion molecule VCAM. Discernible levels of macrophage chemotactic protein 1 (MCP-1), MIF and RANTES were also noted. IBD samples were in companison, rather subdued although II-1 converting enzyme (ICE), TIMP-1, and MIF were notable in all the three different IBD samples examined here. In IBD-4, one of three individual samples, ICE, VCAM, Groa, and MMP expression was more pronounced than in the others.

We also made use of a peripheral blood cDNA library (3) to identify genes expressed by lymphocytes infiltrating the inflamed tissues from the circulating blood. With the 1046element array of randomly selected cDNAs from this library. probes made from RA and IBD samples showed hybridizations to a large number of genes. Of these, many were common between the two disease tissues while others were differentially expressed (data not shown). A complete survey of these genes was beyond the scope of this study, but for this report we picked three genes that were up-regulated in the RA tissue relative to IBD. These cDNAs were sequenced and identified by comparison to the GenBank database. They are TIMP-1, apoferritin light chain, and manganese superoxide dismutase (MnSOD). Differential expression of MnSOD was only observed in samples of RA tissue explants maintained in growth medium without serum for anywhere between 2 to 16 hr. These results also indicate that the expression profile of genes can be altered when explants are transferred to culture conditions.

### DISCUSSION

The speed, ease, and feasibility of simultaneously monitoring differential expression of hundreds of genes with the cDNA microarray based system (1-3) is demonstrated here in the analysis of a complex disease such as RA. Many different cell types in the RA tissue; macrophages, lymphocytes, plasma cells, neutrophils, synoviocytes, chondrocytes, etc. are known to contribute to the development of the disease with the expression of gene products known to be proinflammatory. They include the cytokines, chemokines, growth factors, MMPs, eicosanoids, and others (7, 11-14), and the design of the 96-element known gene microarray was based on this knowledge and depended on the availability of the genes. The technology was validated by confirming earlier observations on the expression of TNF by the monocyte cell line MM6, and of Col-1 and Col-3 expression in the chondrosarcoma cells and articular chondrocytes (9, 12), In our time-dependent survey the chronological order of gene activities in and between gene families was compared and the results have provided unprecedented profiles of the cytokines (TNF, IL-1, IL-6. GCSF, and MIF), chemokines (MIP-1a, MIP-1β, IL-8, and Gro-1), certain transcription factors, and the matrix metalioproteinases (GelA, Strom-1, Col-1, Col-3, HME) in the macrophage cell line MM6 and in the SW1353 chondrosarcoma cells

Earlier reports of cytokine production in the diseased sate had established a model in which ThY is a major participant in RA. Its expression reportedly preceded that of the other cytokines and effector molecules (4). Our results strongly support these results as demonstrated in the time course of the MM6 cells where TNF induction preceded that of IL-1 and IL-Js followed by IL-5 and GCSF. These expression profiles demonstrate the utility of the microarrys in determining the hierarcarby of signaling events.

In the SW1333 chondrosarcoma cells all the known MMPs and TIMPs were examined simultaneously. HME expression was discovered, which previously had been observed in only the stromal cells and alveolar macrophages of smoker's lungs and in placental tissue. Its presence in cells of the RA itsuse is meaningful because its activity can cause significant destruction of elastin and basement membrane components (16, 17). Expression profiles of synovial fibroblasts and articular chondrocytes were remarkably smilar and not too different from the SW1333 cells, indicating that the fibroblast and the chondrocyte can play equally aggressive roles in joint erosion. Prominient genes expressed were

the MMPs, but chemokines and cytokines were also produced by these cells. The effect of the anabolic growth factor TGF-8 was profoundly evident in demonstrating the down regulation of these catabolic activities

RA tissue samples undeniably reflected profiles similar to the cell types examined. Active genes observed were IL-3. IL-6, ICE, the MMPs including HME and TIMPs, chemokines IL-8. Groa, MIP, MIF, and RANTES, and the adhesion molecule VCAM. Of the growth factors, fibroblast growth factor \$\beta\$ was observed most frequently. In comparison, the expression patterns in the other inflammatory state (i.e., IBD) were not as marked as in the RA samples, at least as obtained from the tissue samples selected for this study

As an alternative approach, the 1046 cDNA microarray of randomly selected genes from a lymphocyte library was used to identify genes expressed in RA tissue (3). Many genes on this array hybridized with probes made from both RA and IBD tissue samples. The results are not surprising because inflammatory tissue is abundantly supplied with cell types infiltrating from the circulating blood, made apparent also by the high levels of chemokine expression in RA tissue. Because of the magnitude of the effort required to identify all the hybridized genes, we have for

this report chosen to describe only three differentially expressed genes mainly to verify this method of analysis.

Of the large number of genes observed here, a fair number were already known as active participants in inflammatory dis-ease. These are TNF, IL-1, IL-6, IL-8, GCSF, RANTES, and VCAM. The novel participants not previously reported are HME. IL-3. ICE, and Groα. With our discovery of HME expression in RA, this gene becomes a target for drug intervention. ICE is a cysteine protease well known for its IL-1\beta processing activity (18), and recognized for its role in apoptotic cell death (19). Its expression in RA tissue is intriguing. IL-3 is recognized for its growth-promoting activity in hematopoietic cell lineages, is a product of activated T cells (20), and its expression in synoviocytes and chondrocytes of RA tissue is a novel observation.

Like IL-8, Groa, is a C-X-C subgroup chemokine and is a potent neutrophil and basophil chemoattractant. It downregulates the expression of types I and III interstitial collagens (21, 22) and is seen here produced by the MM6 cells, in primary synoviocytes, and in RA tissue. With the presence of RANTES, MCP, and MIP-18, the C-C chemokines (23) migration and infiltration of monocytes, particularly T cells, into the tissue is also enhanced (5) and aid in the trafficking and recruitment of leukocytes into the RA tissue. Their activation, phagocytosis, degranulation, and respiratory bursts could be responsible for the induction of MnSOD in RA. MnSOD is also induced by TNF and IL-1 and serves a protective function against oxidative damage. The induction of the ferritin light chain encoding gene in this tissue may be for reasons similar to those for MnSOD. Ferritin is the major intracellular iron storage protein and it is responsive to intracellular oxidative stress and reactive oxygen intermediates generated during inflammation (24, 25). The active expression of TIMP-1 in RA tissue, as detected by the 1000-element array, is no surprise because our results have repeatedly shown TIMP-1 to be expressed in the constitutive and induced states of RA cells and tissues.

The suitability of the cDNA microarray technology for profiling diseases and for identifying disease related genes is well documented here. This technology could provide new

targets for drug development and disease therapies, and in doing so allow for improved treatment of chronic diseases that are challenging because of their complexity.

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### Analysis of RNA

A number of methods have been developed to quantitate, measure the size of, and map the 5' and 3' termini of specific mRNA molecules in preparations of cellular RNA. These include:

- Northern hybridization (RNA blotting), in which the size and amount of specific mRNA molecules in preparations of total or poly(A)<sup>-</sup> RNA are determined (Alwine et al. 1977, 1979). The RNA is separated according to size by electrophoresis through a denaturing agarose gel and is then transferred to activated cellulose (Alwine et al. 1977; Seed 1982b), nitrocellulose (Goldberg 1980; Thomas 1980; Seed 1982a), or glass or nylon membranes (Bresser and Gillespie 1983) (see below). The RNA of interest is then located by hybridization with radiolabeled DNA or RNA followed by autoradiography.
- Dot and slot hybridization, in which an excess of radiolabeled probe is
  hybridized to RNA that has been immobilized on a solid support (Kafatos et
  al. 1979; Thomas 1980; White and Bancroft 1982). Densitometric tracings
  of the resulting autoradiographs can allow comparative estimates of the
  amount of the target sequence in various preparations of RNA.
- Mapping RNA using nuclease S1 or ribonuclease, in which the precise positions of the 5' and 3' termini of the mRNA and the locations of splice junctions can be rigorously determined (Berk and Sharp 1977; Weaver and Weissmann 1979). Labeled or unlabeled RNA or DNA probes derived from various segments of the genomic DNA are hybridized to mRNA, often under conditions favoring the formation of DNA:RNA hybrids (Casey and Davidson 1977). The products of the hybridization are then digested with nuclease S1 or RNAase under conditions favoring digestion of singlestranded nucleic acids only. Analysis of the digestion products by gel electrophoresis yields important quantitative and qualitative information about the mRNA structure.
  - Primer extension, in which a small radiolabeled fragment of DNA is hybridized to the mRNA and used as a primer for reverse transcriptase.
     The resulting product should extend to the extreme 5' terminus of the mRNA, and thus the size of the product reflects the number of nucleotides from the position of the label to the 5' terminus of the mRNA.
  - Solution hybridization, in which the absolute concentration of the sequence of interest is calculated from the rate of hybridization of a small amount of a specific radioactive probe with a known quantity of purified cellular RNA (see, e.g., Roop et al. 1978; Durnam and Palmiter 1983). Alternatively, an excess of a radiolabeled probe is incubated with a known amount of RNA. The concentration of the RNA of interest can then be estimated from the amount of radioactivity that becomes resistant to nuclease S1 (see, e.g., Favaloro et al. 1986); Beach and Palmiter 1981; Williams et al. 1986).

Filter hybridization, in which purified cellular RNA is end-labeled with <sup>32</sup>P and hybridized to a large excess of the homologous DNA that has been immobilized on a solid support (Williams et al. 1986).

Below we describe northern hybridization. Dot and slot hybridization of both crude and purified preparations of RNA are described beginning on page 7.53; nuclease-S1 and RNAase analysis of specific hybrids, beginning on page 7.58 and 7.71, respectively; and analysis of mRNA by primer extension, beginning on page 7.79.